

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:06:21 ; Search time 969.74 Seconds  
(without alignments)  
14135.156 Million cell updates/sec

Title: US-09-931-486-111

Perfect score: 471

Sequence: 1 ATCGAAGATCCCGCTTCTT.....CAGATTCCTGGGGTTATAT 471

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	471	100.0	471	6	A48044	A48044 Sequence 11
2	471	100.0	471	6	AR177089	AR177089 Sequence
3	471	100.0	471	6	AX191052	AX191052 Sequence
4	466.2	99.0	528	1	PAE439391	AJ439391 Pseudomon
5	466.2	99.0	11176	1	AE004949	AE004949 Pseudomon
6	466.2	99.0	12065	1	AE004883	AE004883 Pseudomon
7	452.6	96.1	521	1	PAE439389	AJ439389 Pseudomon
8	443.2	94.1	592	1	AF422498	AF422498 Unculture
9	442.2	93.9	531	1	PAE439388	AJ439388 Pseudomon
10	442.2	93.9	660	1	PSEDFC	L28150 Pseudomonas
11	441.2	93.7	498	1	PAE439392	AJ439392 Pseudomon
12	432.2	91.8	490	1	PAE439390	AJ439390 Pseudomon
13	431.8	91.7	659	1	PSEDFB	L28149 Pseudomonas
14	428.6	91.0	659	1	PSEDFB	L28148 Pseudomonas
15	383.2	81.4	10832	1	AE004501	AE004501 Pseudomon
16	383.2	81.4	17712	1	AE004844	AE004844 Pseudomon
17	302.6	64.2	391	1	AF422518	AF422518 Unculture
18	288.8	61.3	477	1	PST390586	AJ390586 Pseudomon
19	285.6	60.6	477	1	PST251909	AJ251909 Pseudomon
20	276.6	58.7	530	1	PST251907	AJ251907 Pseudomon
21	275	58.4	530	1	PST251906	AJ251906 Pseudomon
22	272.6	57.9	499	6	A48047	A48047 Sequence 11
23	272.6	57.9	499	6	AR177092	AR177092 Sequence
24	272.6	57.9	499	6	AX191055	AX191055 Sequence
25	262.8	55.8	486	1	PBA279238	AJ279238 Pseudomon
26	261.2	55.5	485	1	PBA279239	AJ279239 Pseudomon
27	260.6	55.3	528	1	PST251905	AJ251905 Pseudomon
28	259.6	55.1	529	1	PST251904	AJ251904 Pseudomon
29	259.6	55.1	529	1	PST390587	AJ390587 Pseudomon
30	259	55.0	528	1	PST251903	AJ251903 Pseudomon
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32	258.6	54.9	553	1	D87087	D87087 Pseudomonas
33	254.6	54.1	616	1	AF422492	AF422492 Unculture
34	251.6	53.4	529	1	PST251901	AJ251901 Pseudomon
35	251.6	53.4	529	1	PST251902	AJ251902 Pseudomon
36	250.6	53.2	529	1	PST390590	AJ390590 Pseudomon
37	248.2	52.7	560	1	AF356514	AF356514 Pseudomon
38	244.8	52.0	523	1	PST390581	AJ390581 Pseudomon
39	241.4	51.3	522	1	AF127587	AF127587 Pseudomon
40	236	50.1	527	1	AF127586	AF127586 Pseudomon
41	231	49.0	5679	1	AF134704	AF134704 Pseudomon
42	231	49.0	5785	1	PSU65012	U65012 Pseudomonas
43	228.6	48.5	803	1	AF260010	AF260010 Chlamydia
44	225.8	47.9	504	6	A48046	A48046 Sequence 11
45	225.8	47.9	504	6	AR177091	AR177091 Sequence

ALIGNMENTS

RESULT 1	A48044	Sequence 111 from Patent WO9600298.	471 bp	DNA	linear	PAT 07-MAR-1997
LOCUS	A48044					
DEFINITION	A48044					
ACCESSION	A48044					
VERSION	A48044.1	GI:2301906				
KEYWORDS						
SOURCE		unidentified.				
ORGANISM		unclassified.				
REFERENCE		1 (bases 1 to 471)				
AUTHORS		Jannes.G., Rossau.R. and Van.H.H.				
TITLE		SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF				
JOURNAL		EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY				
		Patent: WO 9600298-A 111 04-JAN-1996;				

Pred. No. is the number of results predicted by chance to have a

1. *Journal of the American Medical Association*, 1997; 277: 1001-1005.

QY 241 CACCATCTAAACAATCGTCGAAGCTCAGAAATGAATGTTCTGGATGAACATTGATTT 300  
 Db 241 CACCATCTAAACAATCGTCGAAGCTCAGAAATGAATGTTCTGGATGAACATTGATTT 300  
 QY 301 CTGGCTTTGCACCAAGACTGTTCTTTAAATAATTCGGGTATGATAGTAAGTAACTGA 360  
 Db 301 CTGGCTTTGCACCAAGACTGTTCTTTAAATAATTCGGGTATGATAGTAAGTAACTGA 360  
 QY 361 ATGATCTCTTCTACTGGTGATCATTCAGTCAAGGTAAATAATTCGAGTTCAAGCGGAA 420  
 Db 361 ATGATCTCTTCTACTGGTGATCATTCAGTCAAGGTAAATAATTCGAGTTCAAGCGGAA 420  
 QY 421 TTTTCGGCGAATCTGCTCTTACAGTATAACAGATTGCTTGGGGTTATAT 471  
 Db 421 TTTTCGGCGAATCTGCTCTTACAGTATAACAGATTGCTTGGGGTTATAT 471

RESULT 4  
 PAE439391  
 LOCUS  
 DEFINITION  
 Pseudomonas aeruginosa 16S rRNA gene, 23S rRNA gene, trRNA-Ile gene, trRNA-Ala gene and ITS1, strain EVA8.  
 ACCESSION  
 AJ439391  
 VERSION  
 1  
 KEYWORDS  
 16S ribosomal RNA; 16S rRNA gene; 23S ribosomal RNA; 23S rRNA gene; internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer RNA-Ile; trRNA-Ala gene; trRNA-Ile gene.  
 SOURCE  
 Pseudomonas aeruginosa.  
 ORGANISM  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.

REFERENCE  
 1 Han, R., Min, H., Zhang, C., and Cheng, Z.  
 Comparative analysis of crude oil degrading bacteria on the basis of 16S-23S internal transcribed spacers  
 JOURNAL  
 Unpublished  
 AUTHORS  
 2 (bases 1 to 528)  
 TITLE  
 Direct Submission  
 Submitted (17-MAR-2002) Han R., College of Life Science, Zhejiang University, Hualiang Campus, Hangzhou, Zhejiang, 310029, CHINA  
 JOURNAL  
 Location/Qualifiers  
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 /organism="Pseudomonas aeruginosa"  
 /strain="EVA8"  
 /db\_xref="taxon:287"  
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 rRNA  
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 118. 194  
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 rRNA  
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 Best Local Similarity 99.4%; Pred. No. 2.5e-124;  
 Matches 468; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ATCGAAGATCCCGCTTCTTCAATAAGCTCCACACGAATTCCTTGATCTACTGTTAGAC 60  
 Db 54 ATCGAAGATCTCAGCTTCTTCAATAAGCTCCACACGAATTCCTTGATCTACTGTTAGAC 113  
 QY 61 GATTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATTAAGGGTGAAGTTCGGCAGTT 120  
 Db 114 GATTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATTAAGGGTGAAGTTCGGCAGTT 173  
 QY 121 CGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGCGGTGATCCGATACGGGGCCATAGC 180  
 Db 174 CGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGCGGTGATCCGATACGGGGCCATAGC 233  
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 Db 234 TCAGCTGGGAGAGCGCTGCTTTTCACGCGCAGGAGGTCAGGAGTTCGATCTCCTTGGCTC 293  
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 Db 294 CACCATCTAAACAATTCGTCGAAAGCTCAGAAATGAATGTTCTGGATGAACATTGATTT 353  
 QY 301 CTGGTCTTTGCACCAAGACTGTTCTTTAAATAATTCGGGTATGATAGTAAGTAACTGA 360  
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 QY 361 ATGATCTCTTCTACTGGTGATCATTCAGTCAAGGTAAATAATTCGAGTTCAAGCGGAA 420  
 Db 414 ATGATCTCTTCTACTGGTGATCATTCAGTCAAGGTAAATAATTCGAGTTCAAGCGGAA 473  
 QY 421 TTTTCGGCGAATCTGCTCTTACAGTATAACAGATTGCTTGGGGTTATAT 471  
 Db 474 TTTTCGGCGAATCTGCTCTTACAGTATAACAGATTGCTTGGGGTTATAT 524

RESULT 5  
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 LOCUS  
 DEFINITION  
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 ACCESSION  
 AE004949 AE004091  
 VERSION  
 AE004949.1 GI:9951690  
 KEYWORDS  
 Pseudomonas aeruginosa.  
 SOURCE  
 ORGANISM  
 Pseudomonas aeruginosa.  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.  
 REFERENCE  
 1 (bases 1 to 11176)  
 AUTHORS  
 Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warrenner, P., Hickey, M.J., Brinkman, F.S., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R., Smith, K., Spencer, D., Wong, G.K., Wu, Z. and Paulsen, I.T.  
 Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
 JOURNAL  
 Nature 406 (6799), 959-964 (2000)  
 MEDLINE  
 20437337  
 PUBMED  
 10984043  
 REFERENCE  
 2 (bases 1 to 11176)  
 AUTHORS  
 Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Sailer, M.H., Hancock, R.E.W., Lory, S. and Olson, M.V.  
 Direct Submission  
 Submitted (16-MAY-2000) Department of Medicine and Genetics,

University of Washington Genome Center, University Of Washington,  
Box 352145, Seattle, WA 98195, USA

## FEATURES

## source

1. .11176

/organism="Pseudomonas aeruginosa"

/strain="PA01"

/db\_xref="taxon:287"

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/gene="PA5369"

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/transl\_table=11

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/protein\_id="AAG08754.1"

/db\_xref="GI:9951691"

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TWGLGLGDAKKVQLPGRNSVSTGYFKEALCKDPRNPNEOPGSAVYQSV

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/complement(1877..4767)

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/complement(4994..5069)

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/product="trna-Ile"

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ACGTLSGTAGTLGLSLVATINFSYATVODYAWRIPELILGGVGLFVSVLRRL

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SVYGDALAKANSLAIVCLLGLCIVAGMADRYCAGLITFVAGSVLLALVSWFVGN

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HAMVEAGVQAGVPRTRDNLGQQEGFQGNPDVTAHARREVIVSGATAPOLLQSRGVP  
VTHALSDRILFSGRKRAIGSVLVGNGDNPTAHARREVIVSGATAPOLLQSRGVP  
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LGKGLGASNQEPAGFIITREAFEPNFIQFELPVAIYNGSKGVQEGHGFQAHGMSMR  
SPSRGRIHLKSRDPRQHPHSIILFNYSHEODWQFERDGIKRLTREIMNQPALDPYRGREL  
SPGVSVQSDAELDEFIRHAEFTAFHPSCKRMGSDMAVVGQGRVHGMELRVKVDAS  
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BASE COUNT 2242 a 3417 c 3071 g 2446 t

## ORIGIN

Query Match 99.0%; Score 466.2; DB 1; Length 11176;  
Best Local Similarity 99.4%; Pred. No. 3.7e-124;  
Matches 468; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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DB 5238 ATCGAAGATCTCAGCTCTTCATAAGCTCCACACGAATTCCTTACTGATTCTACTGTTAGAC 5179  
QY 61 GATTGGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGGGTGAGGTGCGGCAATT 120  
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DB 5118 CGAATCTGCCAGACCCACCAATTTGGTGTGCTGCTGATCCGATACGGGGCCATAGC 5059  
QY 181 TCAGCTGGGAGAGCGCTGCTTTCACGACGAGGAGTTCGATTCCTCTCTTGGCTC 240  
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QY 301 CTGGTCTTTGACCAAGAACTGTTCTTTAAATAATTCGGTATGTCATAGAAGTAAAGCTGA 360  
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QY 361 ATGATCTCTTTTCACTGGTGTGATTCATCAAGTCAAGTAAAATTTTCGAGTTTCAAGCGCGAA 420  
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DB 4878 ATGATCTCTTTTCACTGGTGTGATTCATCAAGTCAAGTAAAATTTTCGAGTTTCAAGCGCGAA 4819  
QY 421 TTTTTCGGCGAATGCTGCTTCACAGTAAACCAGATGCTTTGGGTTATAT 471  
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DB 4818 TTTTTCGGCGAATGCTGCTTCACAGTAAACCAGATGCTTTGGGTTATAT 4768

## RESULT 6

AE004883/c

LOCUS

DEFINITION

Pseudomonas aeruginosa PA01, section 444 of 529 of the complete

genome.

ACCESSION

AE004883.1

VERSION

AE004883.1

KEYWORDS

Pseudomonas aeruginosa.

SOURCE

Pseudomonas aeruginosa.

ORGANISM

Pseudomonas.

REFERENCE

1 (bases 1 to 12065)

AUTHORS

Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warrenner, P.,

Hickey, M.J., Brinkman, F.S., Hufnagle, W.O., Kowalik, D.J., Lagrou, M.,

Garber, R.L., Gots, R.L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y.,

Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.,

Smith, K., Spencer, D., Wong, G.K., Wu, Z. and Paulsen, I.T.

Complete genome sequence of Pseudomonas aeruginosa PA01, an

opportunistic pathogen

Nature 406 (6799), 959-964 (2000)

JOURNAL

MEDLINE

PUBMED

10984043

REFERENCE

2 (bases 1 to 12065)

AUTHORS

Stover, C.K., Pham, X.-Q., Erwin, A.L., Mizoguchi, S.D., Warrenner, P.,





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Query Match      96.1%; Score 452.6; DB 1; Length 521;
Best Local Similarity 98.9%; Pred. No. 2.2e-120;
Matches 466; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Db 48 ATCGAAGATCTCAGCTCTTCTTATAGCTCCACACGAAATGCTGTTGATTCAGTCTAGAC 107
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QY 61 GATTGGTCTGTAGCTCAGTCTGTTAGAGCCACCCCTGATAAGGTCAGGTCGSCAGTT 120
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Db 108 GATTGGTCTGTAGCTCAGTCTGTTAGAGCCACCCCTGATAAGGTCAGGTCGSCAGTT 167
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QY 241 CACCATCTAAACAAATCTCGAAGCTCAGAAATCAATGTTCTGATGAACATTTGATTT 300
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RESULT 8
AF422498 592 bp DNA linear BCT 11-JUN-2002
LOCUS Uncultured bacterium clone t1007 16S ribosomal RNA gene, partial
DEFINITION sequence; 16S-23S ribosomal RNA intergenic spacer, complete
ACCESSION AF422498
VERSION AF422498
KEYWORDS uncultured bacterium.
SOURCE uncultured bacterium.
ORGANISM uncultured bacterium.
REFERENCE 1 (bases 1 to 592)
AUTHORS Lowe,M., Madsen,E.L., Schindler,K., Smith,C., Emrich,S., Robb,F.
and Halden,R.U.
TITLE Geochemistry and microbial diversity of a
JOURNAL trichloroethene-contaminated Superfund site undergoing intrinsic in
REFERENCE situ reductive dechlorination
AUTHORS FEMS Microbiol. Ecol. 40 (2), 123-134 (2002)
TITLE 2 (bases 1 to 592)
JOURNAL and Halden,R.U.
REFERENCE Lowe,M.L., Madsen,E.L., Schindler,K., Smith,C., Emrich,S., Robb,F.
AUTHORS Direct Submission
TITLE Submitted (24-SEP-2001) Physics Department, Loyola College in
JOURNAL Maryland, 4501-N. Charles Street, Baltimore, MD 21210, USA
FEATURES Location/Qualifiers
source 1. .592
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/db_xref="taxon:77133"
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intergenic spacer, and 23S ribosomal RNA"
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Best Local Similarity 98.9%; Pred. No. 1.2e-117;
Matches 467; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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Db 57 ATCGAAGATCCCGGCTTCTTCATAAGCTCCACACCAATGCTTGATTCACCTGGTTAGAC 116
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QY 121 CGAATCTGCCAGACCCACCAATGTTGGTGTCTGCGTATCCGATACGGGCCATAGC 180
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Db 177 CGAATCTGCCAGACCCACCAATGTTGGTGTCTGCGTATCCGATACGGGCCATAGC 236
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QY 301 CTGGTCTTTGCCACCAAGACTGTTCTTTAAATTCGGGTATGTGATAGAAGTAAGACTGA 360
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QY 361 ATGATCTCTTTACACGCTGATCAATCAAGTCAAGTAAATTTCCGAGTTCAAGCGGGA 419
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QY 420 ATTTTCGCGAATGTCGCTTTCACAGTATAACCAAGTTCGTTGGGTTATAT 471
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RESULT 9
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DEFINITION
Pseudomonas aeruginosa 16S rRNA gene, 23S rRNA gene, trna-Ile gene,
trna-Ala gene and ITS1, strain EVA5.
ACCESSION
AJ439388
VERSION
AJ439388.1 GI:19692854
KEYWORDS
16S ribosomal RNA; 16S rRNA gene; 23S ribosomal RNA; 23S rRNA gene;
internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer
RNA-Ile; trna-Ala gene; trna-Ile gene.
SOURCE
Pseudomonas aeruginosa.
ORGANISM
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE
1
Han, R., Min, H., Zhang, C. and Cheng, Z.
AUTHORS
Comparative analysis of crude oil degrading bacteria on the basis
TITLE
of 16S-23S internal transcribed spacers
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 531)
Han, R.
AUTHORS
Direct Submission
TITLE
Submitted (17-MAR-2002) Han R., College of Life Science, Zhejiang
JOURNAL
University, Huajiaochi Campus, Hangzhou, Zhejiang, 310029, CHINA
FEATURES
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Best Local Similarity 98.1%; Pred. No. 2.3e-117;
Matches 458; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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QY 61 GATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGTGAGGTGGCGAGTT 120
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QY 121 CGAATCTGCCAGACCCACCAATGTTGGTGTCTGCGTATCCGATACGGGCCATAGC 180
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QY 181 TCAGCTGGGAGAGCGGCTGCTTTGACAGCAGGAGGTTCAGAGTTCGATCCTCTTGGCTC 240
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Db 233 TCAGCTGGGAGAGCGGCTGCTTTGACAGCAGGAGGTTCAGAGTTCGATCCTCTTGGCTC 292
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Db 293 CACCATC-CAAACAATCGTCGAAAGCTCAGAAATGAATGCTTGGTGGATGAACATGATTT 351
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QY 361 ATGATCTCTTTACCTGGTATTCATCAAGTCAAGTAAATTTGCGAGTTCAAGCGGGA 420
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Db 412 ATGATCTCTTTACCTGGTATTCATCAAGTCAAGTAAATTTGCGAGTTCAAGCGGGA 471
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Db 472 TTTTCGCGAATGTCGCTTTCACAGTATAACCAAGTTCGTTGGGTT 518
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## RESULT 10

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LOCUS
DEFINITION
Pseudomonas aeruginosa 16S ribosomal RNA (16S rRNA) gene, transfer
RNA-Ile (trna-Ile) gene, transfer RNA-Ala (trna-Ala) gene, 23S
ribosomal RNA (23S rRNA) gene.
ACCESSION
L28150
VERSION
L28150.1 GI:453540
KEYWORDS
16S ribosomal RNA; 23S ribosomal RNA; trna; transfer RNA.
SOURCE
Pseudomonas aeruginosa
ORGANISM
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.

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REFERENCE 1 (bases 1 to 660)  
 AUTHORS Tyler, S.D., Strathdee, C.A., Rozee, K.R. and Johnson, W.M.  
 TITLE Oligonucleotide primers designed to differentiate pathogenic  
 pseudomonads on the basis of the sequencing of genes coding for  
 16S-23S rRNA internal transcribed spacers  
 JOURNAL Clin. Diagn. Lab. Immunol. 2 (4), 448-453 (1995)  
 MEDLINE 96082422  
 PUBMED 7583922

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 Matches 466; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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 Db 143 ATCGAAGATCCAGCTCTTCTTATAGTCCACACGAAATGCTTGTGATCTACTGTTAGAC 202  
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 QY 61 GATTGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGATAGGGTGAGTCGCGCAGTT 120  
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 QY 121 CGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGCTGATCCGATACGGGGCCATAGC 180  
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 ACCESSION AJ439392  
 VERSION AJ439392.1 GI:19682858  
 KEYWORDS 16S ribosomal RNA; 16S rRNA gene; internal transcribed spacer 1;  
 ITS1; transfer RNA-Ala; transfer RNA-Ile; tRNA-Ala gene; tRNA-Ile  
 gene.  
 SOURCE Pseudomonas aeruginosa.  
 ORGANISM Pseudomonas aeruginosa  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 Pseudomonas.  
 REFERENCE 1  
 AUTHORS Han, R., Min, H., Zhang, C. and Cheng, Z.  
 TITLE Comparative analysis of crude oil degrading bacteria on the basis  
 of 16S-23S internal transcribed spacers  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 498)  
 AUTHORS Han, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-MAR-2002) Han R., College of Life Science, Zhejiang  
 University, Huajiaochi Campus, Hangzhou, Zhejiang, 310029, CHINA  
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 Db 473 TTTTCGGCGAATGTCGCTTCACAGT 498  
  
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 LOCUS  
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 ACCESSION AJ439390  
 VERSION AJ439390.1 GI:19692856  
 KEYWORDS 16S ribosomal RNA; 16S rRNA gene; internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer RNA-Ile; trna-Ala gene; trna-Ile gene.  
 SOURCE Pseudomonas aeruginosa.  
 ORGANISM Pseudomonas aeruginosa  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.  
 REFERENCE 1  
 AUTHORS Han, R., Min, H., Zhang, C. and Cheng, Z.  
 TITLE Comparative analysis of crude oil degrading bacteria on the basis of 16S-23S internal transcribed spacers  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 490)  
 AUTHORS Han, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-MAR-2002) Han R., College of Life Science, Zhejiang University, Huaijiachi Campus, Hangzhou, Zhejiang, 310029, CHINA  
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 Db 114 GATTGGGTCTGTAGCTCAGTGTGGTTAGAGCGCACCCCTGATAAGGTTGAGTTCGCGAGTT 173  
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 QY 421 TTTTCGGCGAATGTCGT 437  
 Db 474 TTTTCGGCGAATGTCGT 490  
  
 RESULT 13  
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 LOCUS  
 DEFINITION Pseudomonas aeruginosa 16S ribosomal RNA (16S rRNA) gene, transfer RNA-Ile (trna-ile) gene, transfer RNA-Ala (trna-Ala) gene, 23S ribosomal RNA (23S rRNA) gene.  
 ACCESSION L28149  
 VERSION L28149.1 GI:453539  
 KEYWORDS 16S ribosomal RNA; 23S ribosomal RNA; trna: transfer RNA.  
 SOURCE Pseudomonas aeruginosa  
 ORGANISM Pseudomonas aeruginosa  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.  
 REFERENCE 1 (bases 1 to 659)  
 AUTHORS Tyler, S.D., Strathdee, C.A., Rozee, K.R. and Johnson, W.M.  
 TITLE Oligonucleotide primers designed to differentiate pathogenic pseudomonads on the basis of the sequencing of genes coding for 16S-23S rRNA internal transcribed spacers  
 JOURNAL Clin. Diagn. Lab. Immunol. 2 (4), 448-453 (1995)  
 MEDLINE 96082422  
 PUBMED 7583922  
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Best Local Similarity 99.2%; Pred. No. 4.5e-100;
Matches 385; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 GATTGGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGGTGAGGTCGGCAGTT 120
Db 10505 GATTGGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGGTGAGGTCGGCAGTT 10564

QY 121 CGAATCTGCCAGACCCACCAATTTGTTGCTGCTGCTGATCCGATACGGGGCCATAGC 180
Db 10565 CGAATCTGCCAGACCCACCAATTTGTTGCTGCTGCTGATCCGATACGGGGCCATAGC 10624

QY 181 TCAGCTGGGAGAGCGCTCTTTCACGACGAGGTCAGGAGTTCGATCCTCTTGGCTC 240
Db 10625 TCAGCTGGGAGAGCGCTCTTTCACGACGAGGTCAGGAGTTCGATCCTCTTGGCTC 10684

QY 241 CACCATCTAAACAATCGTCGAAAGCTCAGAAATGAATGTTGCTGGATGAACATTGATTT 300
Db 10685 CACCATCTAAACAATCGTCGAAAGCTCAGAAATGAATGTTGCTGGATGAACATTGATTT 10744

QY 301 CTGGTCTTTGCACCAAGCTGTTCTTTAAATAATTCGGGTATGTGATAGAGTAAGACTGA 360
Db 10745 CTGGTCTTTGCACCAAGCTGTTCTTTAAATAATTCGGGTATGTGATAGAGTAAGACTGA 10804

QY 361 ATGATCTCTTTTCACCTGGTGATCATTCAA 388
Db 10805 ATGATCTCTTTTCACCTGGTGATCATTCAA 10832
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

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16:	SIDS2/cgcdata/geneseq/geneseq-emb1/NA1995.DAT.*
17:	SIDS2/cgcdata/geneseq/geneseq-emb1/NA1996.DAT.*
18:	SIDS2/cgcdata/geneseq/geneseq-emb1/NA1997.DAT.*
19:	SIDS2/cgcdata/geneseq/geneseq-emb1/NA1998.DAT.*
20:	SIDS2/cgcdata/geneseq/geneseq-emb1/NA1999.DAT.*
21:	SIDS2/cgcdata/geneseq/geneseq-emb1/NA2000.DAT.*
22:	SIDS2/cgcdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23:	SIDS2/cgcdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24:	SIDS2/cgcdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	471	100.0	471	17	AAT11842	P. aeruginosa UZG
2	272.6	57.9	499	17	AAT11845	P. alcaligenes LMG
3	225.8	47.9	504	17	AAT11844	P. stutzeri LMG 23
4	216	45.9	468	17	AAT11846	P. putida LMG 2232
5	183.8	39.0	588	22	AA169774	16S/23S rRNA spacer
6	174	36.9	520	17	AAT11843	p. pseudoalcaligenes
7	113.4	24.1	470	17	AAT11898	Yersinia enterocol
8	104.4	22.2	400	18	AAV78022	Staphylococcus aur
9	104.4	22.2	400	18	AAV77902	Staphylococcus aur

10	104.4	22.2	1311	18	AAV77852
11	103.8	22.0	249	17	AAH51855
12	103	21.9	1396	22	AAH55089
13	103	21.9	2839	22	AAH54998
14	103	21.9	3444	22	AAH54992
15	103	21.9	4429	22	AAH54300
16	101.8	21.6	400	18	AAV77984
17	100	21.2	463	17	AAH1870
18	100	21.2	475	17	AAH11869
19	98.4	20.9	496	17	AAH11866
20	98.4	20.9	1265	24	ABQ69060
21	98.4	20.9	1409	24	ABQ70714
22	98.4	20.9	5015	24	ABQ71078
23	98.2	20.8	5097	20	AAH24983
24	98.2	20.8	5341	20	AAH24986
25	98	20.8	351	18	AAV78405
26	95.2	20.2	640681	24	ABA52787
27	95.2	20.2	2944528	24	ABA303041
28	95	20.2	363	17	AAH11865
29	95	20.2	5105	20	AAH24989
30	94.4	20.0	243	23	AAH48781
31	93.8	19.9	255	23	AAH48800
32	93.8	19.9	255	23	AAH48825
33	93.8	19.9	255	23	AAH48838
34	93.8	19.9	255	23	AAH48846
35	93.8	19.9	255	23	AAH48854
36	93.8	19.9	255	23	AAH48877
37	93.8	19.9	255	23	AAH48882
38	93.8	19.9	255	23	AAH48896
39	93.8	19.9	255	23	AAH48898
40	93.8	19.9	255	23	AAH48967
41	93.8	19.9	255	23	AAH49061
42	93.6	19.9	684707	24	ABQ67196
43	93.6	19.9	3011208	24	ABQ692445
44	93.2	19.8	498	17	AAH11867
45	92.6	19.7	582	12	AAQ14104

## ALIGNMENTS

RESULT 1  
AAT11842

AAT11842  
ID AAT11842 standard: DNA: 471 BP.

XX  
AC AAT11842:

XX 03-SEP-1996 (first entry)

XX  
DE P. aeruginosa UZG 5669 16S-23S rRNA spacer region.

AA Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.

AA  
OS  
Pseudomonas aeruginosa.

AA PN WO9600298-A1.

XX  
PD  
04-JAN-1996.

XX 23-JUN-1995: 95WO-EP02452.

XX 07-APR-1995: 95EP-0870032.

PR 07-APR-1993; 95EF-0870032;  
PR 24-JUN-1994; 94EP-0870106.

PA (INNO-) INNOGENETICS NV.

PI Jannes G, Rossau R, Van Heuverswyn H;

James G. Thompson, Jr.  
XX

WPI; 1996-068882/07.  
XX  
PT Novel hybridisation assay for the detection of eubacteria - esp





Db 121 TAAGGTGAGGTCGGCAGTTTCAATCTGCCAGACCCACCAATT----- 164  
 Qy 161 ATCCGATACCGGGCCATAGCTAGCTGGGAGAGCGCTCTTTCACGAGGAGGTTCAGG 220  
 Db 165 -----TGTGGGGCCATAGCTAGCTGGGAGAGCGCTCTTTCACGAGGAGGTTCAGC 219  
 Qy 221 AGTTGATCTCTTGGCTCCACCATC---TAAACAATCGTGAAGCTCAGAAATGAA 277  
 Db 220 GGTTCGATCCCGTGGCTTCACACCCCGCTTGCAGTTTGTCAAGTTTGAATGAA 279  
 Qy 278 TGTTCGATGAACATGATTTCTGTCTTTCACGAGAGTGTCTTTCACGAGAGTTCGG 337  
 Db 280 TATTCG-CGTCAATATTGATTTCTGAATTT--ATCAGAATCGTCTTTCACGAGAGTTCGG 336  
 Qy 338 GTATGTGATGAGTGAAGTGAATGATCTCTTTCACGAGAGTGTCTTTCACGAGAGTTCGG 397  
 Db 337 GTATGTGATGAGTGAAGTGAATGATCTCTTTCACGAGAGTGTCTTTCACGAGAGTTCGG 396  
 Qy 398 AAATTTGCGAGTTCAAGCGCAATTTTCGCGCAATGCTCTTTCACGAGAGTGTCTTTCACGAGAGTTCGG 457  
 Db 397 AAATTTGTCAGT--AATTACAGTTTTCGCGCAATGCTCTTTCACGAGAGTGTCTTTCACGAGAGTTCGG 454  
 Qy 458 GCTTGGGGTTATAT 471  
 Db 455 GCTTGGGGTTATAT 468

## RESULT 5

AAT169774  
 ID AAT169774 standard; DNA; 588 BP.

XX AAT169774;

DT 13-DEC-2001 (first entry)

XX 16S/23SrRNA spacer region.

DE 16S/23SrRNA spacer region.

XX Bacterium detection; 16S/23SrRNA spacer region; ds.

XX Pseudomonas putida.

XX JP20011000320-1

XX 17-005-2001

PF 13-JAN-2000; 2000JP-0004160.

PR 13-JAN-2000; 2000JP-0004160.

XX (MITO ) MITSUBISHI JUKOGYO KK.

XX WPI; 2001-605311/69.

XX Detection method of Pseudomonas bacteria -

XX Claim 6; Page 7; 11pp; Japanese.

CC The present invention relates to a method for the detection of the

CC present DNA sequence; the 16S/23SrRNA spacer region of Pseudomonas

CC putida. The method can be used to detect Pseudomonas bacteria.

XX Sequence 588 BP; 147 A; 134 C; 153 G; 149 T; 5 other;

SQ Query Match 39.0%; Score 183.8; DB 22; Length 588;

Best Local Similarity 70.5%; Pred. No. 4.7e-51;

Matches 351; Conservative 0; Mismatches 92; Indels 55; Gaps 6;

Qy 1 ATCAGAGATCCCGGCTCTTTCATAGCTCCACACCAATTCGTTGATTCAGTTCAGGTTAGAC 60

Db 63 ATCAGAGATCAGCTGCTGATGAGTCCACACCAATTCGTTGATTCAGTTCAGGTTAGAC 122

Qy 61 G-----AATGGGTCTGTAGCTCAGTTGTTAGAGCGCACCCCTGTATAAGGGT 107

Db 123 CGATCAAGACCTATATAGGTTGTAGCTCAGTTGTTAGAGCGCACCCCTGTATAANGGT 182  
 Qy 108 GAGGTCCGAGTTCGAATCTGCCAGACCCACCAATTCGTTGTTGTTGCTGCTGATCCGAT 167  
 Db 183 GAGGTCCGAGTTCGAATCTGCCAGACCCACCAATTCGTTGTTGTTGCTGCTGATCCGAT 220  
 Qy 168 AGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGTTCAGGATTCGA 227  
 Db 221 GCGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGTTCAGGATTCGA 280  
 Qy 228 TCTCTCTGGTCCACCATCTAACAACATCGTCAAGCTCAGAAATGAATGTTTCGTTGA 287  
 Db 281 TCCCGCTTGGTCCACCATCTGCTGACCTTGATCAAAATCAAAATGAGCATTCGCGTC 340  
 Qy 288 TGAACATTTGATTTCTGCTTTCACGAGAGTTCGTTTTCACGAGAGTTCGTTGATGATA 347  
 Db 341 T-AATGTTGATTTCTGGCTTTTG---TCAGATCGTCTTTCACGAGAGTTCGTTGATGATA 396  
 Qy 348 GAAGTGAAGTGAATGATCTCTTTCACGAGAGTTCGTTTTCACGAGAGTTCGTTGATGATA 407  
 Db 397 GA--TATAGACTCAACACCATCTTTCACGAGAGTTCGTTTTCACGAGAGTTCGTTGATGATA 454  
 Qy 408 GTTC-----AAGCGCAATTTTCGCGCAATTCGTTTTCACGAGAGTTCGTTGATGATA 453  
 Db 455 GTTCTCTCGAAGAGCAACTTTCGCGCAATTTTCGCGCAATTCGTTTTCACGAGAGTTCGTTGATGATA 514  
 Qy 454 GATTGCTTGGGTTATAT 471  
 Db 515 GATTGCTTGGGTTATAT 532

## RESULT 6

AAT11843

ID AAT11843 standard; DNA; 520 BP.

XX AAT11843;

XX 03-SEP-1996 (first entry)

XX P. pseudoalcaligenes LMG 1225 16S-23S rRNA spacer region.

XX Probe; detection; identification; microorganism; amplify;

XX 16S-23S rRNA spacer region; respiratory tract; universal;

XX species-specific; ss.

XX Pseudomonas pseudoalcaligenes.

XX WO9600298-A1.

XX 04-JAN-1996.

XX 23-JUN-1995; 95WO-EP02452.

XX 07-APR-1995; 95EP-0870032.

XX 24-JUN-1994; 94EP-0870106.

XX (INNO-) INNOGENETICS NV.

XX Jannes G., Roseau R., Van Heuverswyn H;

XX WPI; 1996-068882/07.

XX Novel hybridisation assay for the detection of eubacteria - esp

XX Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region

XX Claim 2; Fig 37; 248pp; English.

XX The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer

XX regions derived from various microorganisms. These sequences were

XX used in the method of the invention for the detection and identification

XX of at least one or more microorganisms. The method comprises amplifying

XX the 16S-23S rRNA spacer region and hybridising one or more of the probes







XX 03-SEP-2001 (first entry)  
 DT S. epidermidis genomic polynucleotide sequence SEQ ID NO:4453.  
 DE Staphylococcus epidermidis SRI strain; infection; diagnosis;  
 KW vaccination; endocarditis; ds.  
 KW Staphylococcus epidermidis.  
 OS WO200134809-A2.  
 PN 17-MAY-2001.  
 PD 09-NOV-2000; 2000WO-US30782.  
 PF 09-NOV-1999; 99US-0164258.  
 PR (GLAX ) GLAXO GROUP LTD.  
 PA Kimmerly WJ;  
 PI WPI; 2001-316495/33.  
 DR Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
 XX useful for vaccinating against infections, e.g. endocarditis -  
 XX Claim 8; Page 2187-2188; 2189pp; English.  
 XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.  
 CC (I) and (II) can have antibacterial activity and therefore can be used  
 CC in vaccination. The nucleic acids (I) may be used to produce the  
 CC S. epidermidis polypeptides (II) via the production of vectors  
 CC containing them which are used to produce hosts cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA  
 CC polynucleotide sequences from the present invention. AAH55091 to  
 CC AAH55098 represent oligonucleotide sequences and primers which are used  
 CC in the exemplification of the present invention.  
 CC N.B. The present invention specifically claims all the polynucleotide  
 CC sequences given in the sequence listing of the present specification,  
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
 CC no sequences are present for SEQ ID NO:4455 to 4464.  
 XX  
 XX Sequence 1396 BP; 410 A; 254 C; 319 G; 413 T; 0 other;  
 Query Match 21.9%; Score 103; DB 22; Length 1396;  
 Best Local Similarity 76.8%; Pred. No. 8.6e-24;  
 Matches 142; Conservative 0; Mismatches 35; Indels 8; Gaps 1;  
 QY 62 ATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGCTGAGGTGCGGAGTTC 121  
 DB 642 AATGGCCCTATAGCTCAGCTGGTTAGAGCGCACGCCCTGATAGGCTGAGGTGCGTGGTTC 701  
 QY 122 GAATCTGCCAGACCCACCAATTTGGTGTGCTGCGTGATCCGATACGGGGCCATAGCT 181  
 DB 702 GAGTCCACTTAGGGCCACCAATTAATTTAAACCTTA-----GGGGGCTTAGCT 753  
 QY 182 CAGCTGGGAGAGCGCTCTTTGACGAGGAGGTTCAGGAGTTCGATCTCTCTTGGCTCC 241  
 DB 754 CAGCTGGGAGAGCGCTCTTTGACGAGGAGGTTCAGGAGTTCGATCTCTCTTGGCTCC 813  
 QY 242 ACCAT 246  
 DB 814 ACCAT 818

RESULT 13  
 AAH54998/c  
 ID AAH54998 standard; DNA; 2839 BP.  
 XX  
 AC AAH54998;  
 XX 03-SEP-2001 (first entry)  
 DT S. epidermidis genomic polynucleotide sequence SEQ ID NO:4362.  
 DE Staphylococcus epidermidis SRI strain; infection; diagnosis;  
 KW vaccination; endocarditis; ds.  
 KW Staphylococcus epidermidis.  
 OS WO200134809-A2.  
 PN 17-MAY-2001.  
 PD 09-NOV-2000; 2000WO-US30782.  
 PF 09-NOV-1999; 99US-0164258.  
 PR (GLAX ) GLAXO GROUP LTD.  
 PA Kimmerly WJ;  
 PI WPI; 2001-316495/33.  
 DR Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
 XX useful for vaccinating against infections, e.g. endocarditis -  
 XX Claim 8; Page 2102; 2188pp; English.  
 XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.  
 CC (I) and (II) can have antibacterial activity and therefore can be used  
 CC in vaccination. The nucleic acids (I) may be used to produce the  
 CC S. epidermidis polypeptides (II) via the production of vectors  
 CC containing them which are used to produce hosts cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA  
 CC polynucleotide sequences from the present invention. AAH55091 to  
 CC AAH55098 represent oligonucleotide sequences and primers which are used  
 CC in the exemplification of the present invention.  
 CC N.B. The present invention specifically claims all the polynucleotide  
 CC sequences given in the sequence listing of the present specification,  
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
 CC no sequences are present for SEQ ID NO:4455 to 4464.  
 XX  
 XX Sequence 2839 BP; 669 A; 794 C; 562 G; 814 T; 0 other;  
 Query Match 21.9%; Score 103; DB 22; Length 2839;  
 Best Local Similarity 76.8%; Pred. No. 1.2e-23;  
 Matches 142; Conservative 0; Mismatches 35; Indels 8; Gaps 1;  
 QY 62 ATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGCTGAGGTGCGGAGTTC 121  
 DB 182 AATGGCCCTATAGCTCAGCTGGTTAGAGCGCACGCCCTGATAGGCTGAGGTGCGTGGTTC 1769  
 QY 122 GAATCTGCCAGACCCACCAATTTGGTGTGCTGCGTGATCCGATACGGGGCCATAGCT 181  
 DB 1768 GAGTCCACTTAGGGCCACCAATTAATTTAAACCTTA-----GGGGGCTTAGCT 1717  
 QY 182 CAGCTGGGAGAGCGCTCTTTGACGAGGAGGTTCAGGAGTTCGATCTCTCTTGGCTCC 241  
 DB 1716 CAGCTGGGAGAGCGCTCTTTGACGAGGAGGTTCAGGAGTTCGATCTCTCTTGGCTCC 1657



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OY 242 ACCAT 246
Db 1656 ACCAT 1652

RESULT 14
AAH54992
XX AAH54992 standard; DNA; 3444 BP.
AC AAH54992;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4356.
XX
KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
KW vaccination; endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
XX 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAX ) GLAXO GROUP LTD.
XX
PI Kimmerly WJ;
XX
DR WPI; 2001-316495/33.
XX
XX
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis -
XX
XX Claim 8; Page 2096-2097; 2188pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
XX (I) and (II) can have antibacterial activity and therefore can be used
XX in vaccination. The nucleic acids (I) may be used to produce the
XX S. epidermidis polypeptides (II) via the production of vectors
XX containing them which are used to produce hosts cells which express the
XX polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX used to vaccinate subjects and to raise antibodies against the bacteria.
XX The polypeptides may also be used to assay for other inhibitors of their
XX activity and therefore identify compounds that may be used for the
XX treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
XX AAH5090 represent specifically claimed S. epidermidis genomic DNA
XX polynucleotide sequences from the present invention. AAH5091 to
XX AAH5098 represent oligonucleotide sequences and primers which are used
XX in the exemplification of the present invention.
XX N.B. The present invention specifically claims all the polynucleotide
XX sequences given in the sequence listing of the present specification,
XX however the sequence listing only goes up to SEQ ID NO:4454 so even
XX though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
XX no sequences are present for SEQ ID NO:4455 to 4464.
XX
XX Sequence 3444 BP; 1203 A; 597 C; 723 G; 921 T; 0 other;
XX
XX Query Match 21.9%; Score 103; DB 22; Length 3444;
XX Best Local Similarity 76.8%; Pred. No. 1.4e-23;
XX Matches 142; Conservative 0; Mismatches 35; Indels 8; Gaps 1;
XX
OY 62 ATTGGCTGTAGCTCAGTGTAGAGCGCACCCCTGATAGGTTGAGTTCGGCAGTTC 121
Db 2708 AATGGCCCTAGTCTACGTGTAGAGCGCACCGCTGATAGGTTGAGTTCGGTTC 2767
OY 122 GAATCTGCCAGACCCACCAATTGTTGGTGTGCTGCGTGATCCGATACGGGCCATAGCT 181
Db 2768 GAGTCCACTTAGGCCACCATCAATATTAARACCTTA-----GGGGGCTTAGCT 2819
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OY 182 CAGCTGGGAGAGCGCTCTTGCAGCGAGGAGTTCAGATCTCCTTGGCTCC 241
Db 2820 CAGCTGGGAGAGCGCTCTTGCAGCGAGGAGTTCAGATCTCCTTGGCTCC 2879

OY 242 ACCAT 246
Db 2880 ACCAT 2884

RESULT 15
AAH54300
ID AAH54300 standard; DNA; 4429 BP.
XX
XX AAH54300;
AC AAH54300;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3664.
XX
KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
KW vaccination; endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
XX 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAX ) GLAXO GROUP LTD.
XX
PI Kimmerly WJ;
XX
DR WPI; 2001-316495/33.
XX
XX
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis -
XX
XX Claim 8; Page 1270-1272; 2188pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
XX (I) and (II) can have antibacterial activity and therefore can be used
XX in vaccination. The nucleic acids (I) may be used to produce the
XX S. epidermidis polypeptides (II) via the production of vectors
XX containing them which are used to produce hosts cells which express the
XX polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX used to vaccinate subjects and to raise antibodies against the bacteria.
XX The polypeptides may also be used to assay for other inhibitors of their
XX activity and therefore identify compounds that may be used for the
XX treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
XX AAH5090 represent specifically claimed S. epidermidis genomic DNA
XX polynucleotide sequences from the present invention. AAH5091 to
XX AAH5098 represent oligonucleotide sequences and primers which are used
XX in the exemplification of the present invention.
XX N.B. The present invention specifically claims all the polynucleotide
XX sequences given in the sequence listing of the present specification,
XX however the sequence listing only goes up to SEQ ID NO:4454 so even
XX though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
XX no sequences are present for SEQ ID NO:4455 to 4464.
XX
XX Sequence 4429 BP; 1327 A; 928 C; 1004 G; 1170 T; 0 other;
XX
XX Query Match 21.9%; Score 103; DB 22; Length 4429;
XX Best Local Similarity 76.8%; Pred. No. 1.6e-23;
XX Matches 142; Conservative 0; Mismatches 35; Indels 8; Gaps 1;
XX
OY 62 ATTGGCTGTAGCTCAGTGTAGAGCGCACCCCTGATAGGTTGAGTTCGGCAGTTC 121
Db 2708 AATGGCCCTAGTCTACGTGTAGAGCGCACCGCTGATAGGTTGAGTTCGGTTC 2767
OY 122 GAATCTGCCAGACCCACCAATTGTTGGTGTGCTGCGTGATCCGATACGGGCCATAGCT 181
Db 2768 GAGTCCACTTAGGCCACCATCAATATTAARACCTTA-----GGGGGCTTAGCT 2819
```

Db 2768 AATGGCCTATAGCTCAGCTGGTTAGAGCGCACGCCTGATAAGCGTGAGGTCGGTGGTTC 2827  
QY 122 GAATCTGCCAGACCCACCAATGTTGGTCTGCTGGTGATCCGATACGGGGCCATAGCT 181  
Db 2828 GAGTCCACTTAGGCCCCACCATTCAATAATTAAACCTTA-----GGGGGCTTAGCT 2879  
QY 182 CAGCTGGGAGAGCGCCTGCTTTGCACGCAGGAGGTCAGGAGTTCGATCCTCCTTGGCTCC 241  
Db 2880 CAGCTGGGAGAGCGCCTGCTTTGCACGCAGGAGGTCAGGAGTTCGATCCTCCTCCTAGTCTCC 2939  
QY 242 ACCAT 246  
Db 2940 ACCAT 2944

Search completed: February 1, 2003, 01:29:11  
Job time : 122.532 secs



; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-765-332-111

Query Match 100.0%; Score 471; DB 3; Length 471;

Best Local Similarity 100.0%; Pred. No. 5.5e-156;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGATCCCGGCTCTTCATAAGCTCCACACGAAATGCTTGAATCACTGTTAGAC 60  
DB 1 ATCGAAGATCCCGGCTCTTCATAAGCTCCACACGAAATGCTTGAATCACTGTTAGAC 60  
QY 61 GATTGGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCCGCGAGTT 120  
DB 61 GATTGGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCCGCGAGTT 120  
QY 121 CGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGGTGTATCGGATACGCGGCGCATAGC 180  
DB 121 CGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGGTGTATCGGATACGCGGCGCATAGC 180  
QY 181 TCAGCTGGGAGAGCGCTGTTTCACGCGAGGAGGTTCAGAGTTCGATCCTCTGGCTC 240  
DB 181 TCAGCTGGGAGAGCGCTGTTTCACGCGAGGAGGTTCAGAGTTCGATCCTCTGGCTC 240  
QY 241 CACATCTAAACAAATCGTGAAGCTCAGAAATGAATGTTGCTGGATGAACATTTGATTT 300  
DB 241 CACATCTAAACAAATCGTGAAGCTCAGAAATGAATGTTGCTGGATGAACATTTGATTT 300  
QY 301 CTGGCTTTGACACAGAACTGTTCTTTAAATAATTCGGGTATGATGAAGTAAGACTGA 360  
DB 301 CTGGCTTTGACACAGAACTGTTCTTTAAATAATTCGGGTATGATGAAGTAAGACTGA 360  
QY 361 ATGATCTCTTCACTGGTGATCATTCAGTCAAGTAAATTTCCGAGTTCAAGCGCGAA 420  
DB 361 ATGATCTCTTCACTGGTGATCATTCAGTCAAGTAAATTTCCGAGTTCAAGCGCGAA 420  
QY 421 TTTTCGGCGAATGCTGCTTTCACAGTATAACAGATTGCTTGGGGTTATAT 471  
DB 421 TTTTCGGCGAATGCTGCTTTCACAGTATAACAGATTGCTTGGGGTTATAT 471

## RESULT 2

US-09-448-894-111

; Sequence 111, Application US/09448894

; Patent No. 6312903

; GENERAL INFORMATION:

APPLICANT: JANNES, GEERT

ROSSAU, RUDI

VAN HEUVERSWYN, HUGO

TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION

AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A

HYBRIDIZATION ASSAY

NUMBER OF SEQUENCES: 216

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHUYE P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/448,894

FILING DATE: 29-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

24-JUN-1994

; APPLICATION NUMBER: 08/765,332  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 111:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 471 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:  
US-09-448-894-111

Query Match 100.0%; Score 471; DB 4; Length 471;

Best Local Similarity 100.0%; Pred. No. 5.5e-156;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGATCCCGGCTCTTCATAAGCTCCACACGAAATGCTTGAATCACTGTTAGAC 60  
DB 1 ATCGAAGATCCCGGCTCTTCATAAGCTCCACACGAAATGCTTGAATCACTGTTAGAC 60  
QY 61 GATTGGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCCGCGAGTT 120  
DB 61 GATTGGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCCGCGAGTT 120  
QY 121 CGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGGTGTATCGGATACGCGGCGCATAGC 180  
DB 121 CGAATCTGCCAGACCCACCAATTTGTTGGTGTGCTGGTGTATCGGATACGCGGCGCATAGC 180  
QY 181 TCAGCTGGGAGAGCGCTGTTTCACGCGAGGAGGTTCAGAGTTCGATCCTCTGGCTC 240  
DB 181 TCAGCTGGGAGAGCGCTGTTTCACGCGAGGAGGTTCAGAGTTCGATCCTCTGGCTC 240  
QY 241 CACATCTAAACAAATCGTGAAGCTCAGAAATGAATGTTGCTGGATGAACATTTGATTT 300  
DB 241 CACATCTAAACAAATCGTGAAGCTCAGAAATGAATGTTGCTGGATGAACATTTGATTT 300  
QY 301 CTGGCTTTGACACAGAACTGTTCTTTAAATAATTCGGGTATGATGAAGTAAGACTGA 360  
DB 301 CTGGCTTTGACACAGAACTGTTCTTTAAATAATTCGGGTATGATGAAGTAAGACTGA 360  
QY 361 ATGATCTCTTCACTGGTGATCATTCAGTCAAGTAAATTTCCGAGTTCAAGCGCGAA 420  
DB 361 ATGATCTCTTCACTGGTGATCATTCAGTCAAGTAAATTTCCGAGTTCAAGCGCGAA 420  
QY 421 TTTTCGGCGAATGCTGCTTTCACAGTATAACAGATTGCTTGGGGTTATAT 471  
DB 421 TTTTCGGCGAATGCTGCTTTCACAGTATAACAGATTGCTTGGGGTTATAT 471

## RESULT 3

US-08-765-332-114

; Sequence 114, Application US/08765332

; Patent No. 6025132

; GENERAL INFORMATION:

APPLICANT: JANNES, GEERT

ROSSAU, RUDI

VAN HEUVERSWYN, HUGO

TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION

AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A

HYBRIDIZATION ASSAY



Db 1 ATCGAAGACTTCAGTCTCTTTCATAAGTTCACACAGCAATTCGTTGATTCATCTGCGGAAA 60  
QY 58 -----GACGATTGGTCTGTAGCTCAGTTCAGTTGGTTAGAGCGCA 93  
Db 61 GCGATTGGTTGAGACCGGAGAGTACGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
QY 94 CCCTGTATAAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGTGTG 153  
Db 121 CCCTGTATAAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGGATG 180  
QY 154 CTGGGTATCCGATACGGGCGCATAGCTCAGCTGGGAGAGCGGCTGTTTGCACGAGGA 213  
Db 181 GCAGTG---TCAAAATGGGCGCATAGCTCAGCTGGGAGAGCGGCTGTTTGCACGAGGA 237  
QY 214 GGTCCAGAGTTCGATCCTCTGGCTCCACCATCTA-AAACAATCGTCGAAAGCTCAGAA 272  
Db 238 GGTCCAGAGTTCGATCCTCTGGCTCCACCATCACTCAGATCGCTGAAAGCTCAGAA 297  
QY 273 ATGAATGTTGCGTGGATGAACATGATTCTGTGCTTTTGCACCAAGAACTGTTCTTAAAAA 332  
Db 298 ATGAACATTTGGTATGTTCAATGTTGATTCTGTGCTTTTGGCCAGAACTGTTCTTAAAAA 357  
QY 333 TTGCGGTATCTGATAGAGTAAGACTGAATGATCTCTTTCACCTGGTGAATCAATTCAGTCA 392  
Db 358 TTGGGTATGTGATAGAGTGA---CTAACAGCGTGTTCACCTGCACGTTGTT--AATCA 412  
QY 393 AGTAAATTTGGGAGTTCGAAGCGCAATTTTTCGGCGAATGCTGCTCTCAC-----A 444  
Db 413 AGCAAAATTTGGGAGTTCGAAGCGCAATTTTTCGGCGAATGCTGCTCTCAC-----A 444  
QY 445 GTATAACAGATGCTTGGGGTTATAT 471  
Db 473 CTATAACAGATGCTTGGGGTTATAT 499

## RESULT 5

US-08-765-332-113  
; Sequence 113, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765.332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994

; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 113:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 504 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-765-332-113  
  
Query Match 47.9%; Score 225.8; DB 3; Length 504;  
Best Local Similarity 75.1%; Pred. No. 1.1e-69;  
Matches 396; Conservative 0; Mismatches 52; Indels 79; Gaps 6;  
  
QY 1 ATCGAAGATCCCGGCTTCTTCATAAGCTCCACACAGCAATTCGTTGATTCATCTGTTAG-- 58  
Db 1 ATCGAAGACACCGGCTTCGTCATAAGCTCCACACAGCAATTCGTTGATTCATCTGCGAAAG 60  
QY 59 -----ACGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 93  
Db 61 GCGATTGGGTTTAGACCCGAGATAAGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA 120  
QY 94 CCCTGTATAAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTTGGTGTG 153  
Db 121 CCCTGTATAAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTCG----- 172  
QY 154 CTGCGGTATCCGATACGGGCGCATAGCTCAGCTGGGAGAGCGGCTGCTTTCACGACGAGGA 213  
Db 173 -----AAGGGGCGCATAGCTCAGCTGGGAGAGCGGCTGCTTTCACGACGAGGA 218  
QY 214 GGTCCAGAGTTCGATCCTCTGGCTCCACCATCTAAACAATCGTCGAAAGCTCAGAAA 273  
Db 219 GGTCCAGGTTTCGATCCCGCTTGGCTCCACCATTAATCTAGTCGCGGAAAGCTCAGAAA 278  
QY 274 TGAATGTT-----CGTGGATGAACATTCGTTCTGCTTTGCA 312  
Db 279 TGAGTGTTCACAGGATGAGTTGATTGCTGGGTTGAACATTCGTTCTGAGCTTGGC 338  
QY 313 CCAGAACTGTTCTTTAAAAATTCGGGTATGTATAGAACTGATGATGATCTCTTC 372  
Db 339 CCAGAACTGTTCTTTAAAAATTTGGGTATGTATAGAACT--AGACCGGATGTTGCTTTC 397  
QY 373 ACTGGTGTATCATTCAGTCAAGTAAATTTGCGAGTTC--AAGCGGCAATTTTCGCGGAA 431  
Db 398 ACTGGCAGCATGTCGGCTCAAGGTAATAATTTGCGTCTTCTATGCAAAATTTTCGCGGAA 457  
QY 432 TGTGCTCTTCACAGTA-----TAACAGATTCGTTGGGGTTATAT 471  
Db 458 TGTGCTCTTCACGTTATAGACAGTAACAGATTCGTTGGGGTTATAT 504  
  
RESULT 6  
US-09-448-894-113  
; Sequence 113, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.

```
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448.894
FILING DATE: 29-NOV-1999
CLASSIFICATION: <Unknown>
07-APR-1995
24-JUN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,332
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95870032.0
FILING DATE: 07-APR-1995
APPLICATION NUMBER: EP 94870106.5
FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-14
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-09-448-894-113

Query Match 47.9%; Score 225.8; DB 4; Length 504;
Best Local Similarity 75.1%; Pred. No. 1.1e-69;
Matches 396; Conservative 0; Mismatches 52; Indels 79; Gaps 6;

QY 1 ATCGAAGATCCCGGCTTCTTCATAGCTCCACAGAAATGCTTGAATCACTGGTTAG-- 58
DB 1 ATCGAAGACACCGGCTTCGTATAAGCTCCACAGAAATGCTTGAATCACTGGCGAAG 60
QY 59 -----ACGATTGGGCTGTAGCTCAGTTCAGTTGGTTAGACGCA 93
DB 61 GCGATTGGGTTTAGACCCAGAGTAGAGATTGGGCTGTAGCTCAGTTGGTTAGACGCA 120
QY 94 CCCCTGATAAGGTGAGGTCGCGAGTTCGAATTCGCCAGACCCCAATTTGTTGGTGTG 153
DB 121 CCCCTGATAAGGTGAGGTCGCGAGTTCGAATTCGCCAGACCCCAATTCG----- 172
QY 154 CTGCGTGATCCGATACGGGGCCATAGCTCAGCTGGGAGAGCGCTTTGCCACGACGA 213
DB 173 -----AAGGGGCCATAGCTCAGCTGGGAGAGCGCTTTGCCACGACGA 218
QY 214 GGTGAGGATTCGATCCTCTTGGCTCCACCATCTAAAACAATCGTCGAAAGCTCAGAAA 273
DB 219 GGTGAGGATTCGATCCTCTTGGCTCCACCATCTAAAACAATCGTCGAAAGCTCAGAAA 278
QY 274 TGAATGTT-----CGTGGATGAACATTAATTTCTGGTCTTTGCA 312
DB 279 TGAGTGTATACGAGGATGAGTTGATTCGCTGGGTTGAACATTAATTTCTGGACTTTCG 338
QY 313 CCAGAACTGTTCTTTAAATAATTCGGGTATGTGATAGAACTGAATGATCTCTTTC 372
DB 339 CCAGAACTGTTCTTTAAATAATTCGGGTATGTGATAGAACTGAATGATCTCTTTC 397
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QY 373 ACTGCTGATCATTCAGTCAAGTAAATTTCCGAGTTC-AAGCCGAATTTTCGGCGAA 431  
DB 398 ACTGGCAGCATGTCGCTCAAGGTAATAATTTCCGCTTCTCTATGCAAAATTTTCGGCGAA 457  
QY 432 TGTCGCTTTCACAGTA-----TAACCAGATTGCTTGGGGTTATAT 471  
DB 458 TGTCGCTTTCACAGTATATAGACAGTACAGATTGCTTGGGGTTATAT 504

RESULT 7  
US-08-765-332-115  
; Sequence 115, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-765-332-115

Query Match 45.9%; Score 216; DB 3; Length 468;  
Best Local Similarity 74.9%; Pred. No. 3.1e-66;  
Matches 370; Conservative 0; Mismatches 75; Indels 49; Gaps 6;

QY 1 ATCGAAGATCCCGGCTTCTTCATAGCTCCACAGAAATGCTTGAATCACTGGTTAG- 59  
DB 1 ATCGAGACATACGCTGCTCATAAGCTCCACAGAAATGCTTGAATCACTGGTTAG- 60







Db 61 AATGCTGTAACGCGACCGCTGTATAGTCTCTAGCTCAGTTGGTTAGAGCCACCCCTG 120  
Qy 100 ATAAGGTTGAGTCCGCGAGTTCGAATCTGCCAGACCCACCAATTTGGTGTGCTGCTG 159  
Db 121 ATAAGGTTGAGTCCGCGAGTTCGAATCTGCCAGACCCACCAATTTGGTGTGCTGCTG 179  
Qy 160 GATCCGATACGCGGCGATAGTCTAGCTGGGAGAGCGCTCTTTCACGCGAGGAGTCCAG 219  
Db 180 -----AATACGGGCGATAGTCTAGCTGGGAGAGCGCTCTTTCACGCGAGGAGTCCAG 234  
Qy 220 GAGTTCGATCTCTTTCGCTCCACA-----TCTAAACAATCTCGAAGAGTCA 269  
Db 235 CGGTTTCGATCCGCTTGGCTCCACACCTCTCTCGTGTGCGGTGATGCTTAAAGAGTTCA 294  
Qy 270 GAAATGA-----ATGTTCTGTGATGAACATGATTTCTGGTCTTT-----CCA 312  
Db 295 GAAATGATGCGGCTTCAGTTTGTCTCTGTTGAGTCTGATTTCTGTTTGTACCGGTA 354  
Qy 313 CCAGAACTGTTCTTTAAATTCGGGTATGTATAGAGTAAAGTGAATGATCTCTTTTC 372  
Db 355 CGAAATCGTTCTTTAAATTCGGGTATGTATAGAGT--GACTGATTAATTCCTTC 412  
Qy 373 ACTGGTATCATCAAGTCAAGTAAATTTG--CGAGTTCAAGCGGCAATTTTCGGCGA 430  
Db 413 ACTGGCAATGATCTGGTCAAGTAAATTTGTTAGTCTCAAGACGCAATTTTCGGCGA 472  
Qy 431 ATGCTGCTTCCAC-----AGTATAACGAGATGCTTGGGTTATAT 471  
Db 473 ATGCTGCTTCCAGGATGAGACAGTAAACGAGATGCTTGGGTTATAT 520

## RESULT 11

US-08-765-332-195  
; Sequence 195, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 195:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 470 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-765-332-195

Query Match 24.1%; Score 113.4; DB 3; Length 470;  
Best Local Similarity 73.1%; Pred. No. 3.9e-30;  
Matches 163; Conservative 0; Mismatches 51; Indels 9; Gaps 1;

Qy 64 TGGGTCCTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGCGACTTCA 123  
Db 75 TAGGCTTCTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGCGACTTCA 134  
Qy 124 ATCTGCCAGACCCACCAATTTGGTGTG-----CTGCGTGTATCCGATACGGGCG 174  
Db 135 GTCCACTCAGGCTACCACTTCTCGAAGTGGAAAAAGTACTGCACGTGACTGTATGGGCG 194  
Qy 175 CATAGCTCAGCTGGGAGAGCGCTGCTTTGACCGAGGTCAGAGGTCGATCCTCT 234  
Db 195 TATAGCTCAGCTGGGAGAGCGCTGCTTTGACCGAGGTCAGAGGTCGATCCTCT 254  
Qy 235 TGGTCCACCATCTAAACAATCTGTCGAAAGCTCAGAAATGAA 277  
Db 255 TAGTCCACCATATAGTCTCTATTTCATCTTCAATCTTCAAGAGTGTA 297

## RESULT 12

US-09-448-894-195  
; Sequence 195, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/448,894  
; FILING DATE: 29-NOV-1999  
; CLASSIFICATION: <Unknown>  
; 07-APR-1995  
; 24-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/765,332  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 195:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 470 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 195:  
US-09-448-894-195

Query Match 24.1%; Score 113.4; DB 4; Length 470;  
Best Local Similarity 73.1%; Pred. No. 3.9e-30;  
Matches 163; Conservative 0; Mismatches 51; Indels 9; Gaps 1;  
QY 64 TGGGCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAGGGTGGAGTGGCGAGTTGGA 123  
Db 75 TAGGCTTGTAGCTAGGTTGGTTAGAGCGCACCCCTGTGATAGGGTGGAGTGGCGAGTTGGA 134  
QY 124 ATCTGCCAGACCCACCAATTGTTGGTGTG-----CTGCGTGTATCCGATACGGGGC 174  
Db 135 GTCCACTCAGGCTACCACTTCTCGAAGTGGAAAGGTAAGTGTGACGTGATGTTGGGGC 194  
QY 175 CATAGCTCAGCTGGGAGAGCGCTGTTTGCACGAGGAGTTCAGAGTTCGATCCTCT 234  
Db 195 TATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGAGTTCGATCCTCT 254  
QY 235 TGGCTCCACCTATAAACAATCGTGAAGCTCAGAAATGAA 277  
Db 255 TAGCTCCACCATATATCTCTGTATTTCAATACTTCAGAGTGTA 297

RESULT 13  
US-08-765-332-128  
; Sequence 128, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 128:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-128

Query Match 22.0%; Score 103.8; DB 3; Length 249;  
Best Local Similarity 76.2%; Pred. No. 6.5e-27;  
Matches 144; Conservative 0; Mismatches 37; Indels 8; Gaps 1;  
QY 65 GGGTCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAGGGTGGAGTGGCGAGTTGGA 124  
Db 61 GGGTCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAGGGTGGAGTGGCGAGTTGGA 120  
QY 125 TCTGCCAGACCCACCAATTGT-----TGGTGTCTGCTGCTGATCCGATACGGGGCCA 176  
Db 121 TCTTGTTCAGACCCCAAAATCTGAAGATATGTCGTTCAFTATGATTTAAAGCTGGGGACT 180  
QY 177 TAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGAGTTCGATCCTCTCTTG 236  
Db 181 TAGCTTGTGGTAGAGCGCTGCTTTCACGACGAGGAGTTCAGAGTTCGACTCTCTCTAG 240  
QY 237 GCTCCACCA 245  
Db 241 TCTCCACCA 249

RESULT 14  
US-09-448-894-128  
; Sequence 128, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/448,894  
; FILING DATE: 29-NOV-1999  
; CLASSIFICATION: <Unknown>  
; 07-APR-1995  
; 24-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/765,332

; FILING DATE: <Unknown>  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 128:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 249 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 128:  
US-09-448-894-128

Query Match 22.0%; Score 103.8; DB 4; Length 249;  
Best Local Similarity 76.2%; Pred. No. 6.5e-27;  
Matches 144; Conservative 0; Mismatches 37; Indels 8; Gaps 1;  
QY 65 GGGTCGTAGCTAGCTAGGCGCACCCCTGATAAGGTGAGTGGCGCAGTTCGAA 124  
Db 61 GGGTCGTAGCTAGCTAGGCGCACCCCTGATAAGGTGAGTGGCGCAGTTCGAA 120  
QY 125 TCTGCCACAGCCACCAATTGT-----TGGTGTGCTGCTGATCCGATACGGGGCCA 176  
Db 121 TCTTGTACAGCCACCAATCTGAAAGATATGCTGTTTATGATTAAGCTGGGGACT 180  
QY 177 TAGCTCAGCTGGAGAGCGCTGCTTTGACGACGAGGTGAGTTCGATCCCTCTTG 236  
Db 181 TAGCTTAGTGTAGAGCGCTGCTTTGACGACGAGGTGAGTTCGATCCCTCTTG 236  
QY 237 GCTCCACCA 245  
Db 241 TCTCCACCA 249

RESULT 15  
US-08-765-332-215  
; Sequence 215, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 215:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 463 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-765-332-215

Query Match 21.2%; Score 100; DB 3; Length 463;  
Best Local Similarity 75.0%; Pred. No. 2e-25;  
Matches 141; Conservative 0; Mismatches 40; Indels 7; Gaps 1;  
QY 65 GGGTCGTAGCTAGCTAGGCGCACCCCTGATAAGGTGAGTGGCGCAGTTCGAA 124  
Db 115 GGGCTATAGCTAGCTAGGCGCACCCCTGATAAGGTGAGTGGCGCAGTTCGAG 174  
QY 125 TCTGCCACAGCCACCAATTGTGCTGCTGCTGATCCG-----ATACGGGGCCAT 177  
Db 175 TCCACTTAGGCCCACTTTTGAATAAACCTTTCTTTTATATGTTAATAAGGGCCCT 234  
QY 178 AGCTCAGCTGGGAGAGCGCTGCTTTGACGAGGAGTTCAGAGTTCGATCCTCCTTG 237  
Db 235 AGCTCAGCTGGGAGAGCGCTGCTTTGACGAGGAGTTCAGAGTTCGATCCTCCTTG 294  
QY 238 CTCCACCA 245  
Db 295 CTCCACCA 302

Search completed: February 1, 2003, 04:24:12  
Job time : 26.4874 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 03:05:22 ; Search time 26.2092 Seconds  
(without alignments)  
8073.649 Million cell updates/sec

Title: US-09-931-486-111

Perfect score: 471

Sequence: 1 ATCGAAGATCCGGCTCTT.....CAGATTGCTGGGGTTATAT 471

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PC1\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
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- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	95.2	20.2	640681	10	US-09-790-988-1
2	94.4	20.0	243	10	US-09-815-242-1358
3	93.8	19.9	255	10	US-09-815-242-1377
4	93.8	19.9	255	10	US-09-815-242-1402
5	93.8	19.9	255	10	US-09-815-242-1415
6	93.8	19.9	255	10	US-09-815-242-1423
7	93.8	19.9	255	10	US-09-815-242-1431
8	93.8	19.9	255	10	US-09-815-242-1454
9	93.8	19.9	255	10	US-09-815-242-1459
10	93.8	19.9	255	10	US-09-815-242-1473
11	93.8	19.9	255	10	US-09-815-242-1475
12	93.8	19.9	255	10	US-09-815-242-1544
13	93.8	19.9	255	10	US-09-815-242-1638
14	92.6	19.7	582	10	US-09-863-086-87
15	92.6	19.7	590	10	US-09-863-086-88
16	87.2	18.5	3309400	9	US-09-738-626-1
17	85.2	18.1	549	10	US-09-863-086-92
18	82.6	17.5	498	10	US-09-863-086-90
19	81.8	17.4	603	10	US-09-863-086-85

20	81.8	17.4	603	10	US-09-863-086-86
21	68.6	14.6	836	9	US-09-894-467-5
22	66.4	14.1	76	10	US-09-974-300-4361
23	66.4	14.1	76	10	US-09-974-300-4403
24	66.4	14.1	76	10	US-09-974-300-4409
25	66.4	14.1	76	10	US-09-974-300-4418
26	66.4	14.1	76	10	US-09-974-300-8396
27	66.4	14.1	76	10	US-09-974-300-8438
28	66.4	14.1	76	10	US-09-974-300-8444
29	66.4	14.1	76	10	US-09-974-300-8453
30	66.4	14.1	290	10	US-09-815-242-4692
31	66.4	14.1	495	10	US-09-815-242-2687
32	66.4	14.1	495	10	US-09-815-242-2691
33	65.8	14.0	1069	10	US-09-070-927A-869
34	65.4	13.9	279	10	US-09-863-086-96
35	64.8	13.8	9797	10	US-09-070-927A-550
36	64.8	13.7	2336	10	US-09-842-552-102
37	64.4	13.7	74	10	US-09-974-300-4363
38	64.4	13.7	76	10	US-09-974-300-8398
39	63.8	13.5	246	10	US-09-863-086-95
40	62.8	13.3	654	10	US-09-863-086-89
41	61.6	13.1	1883	10	US-09-927-483-3
42	61.6	13.1	1883	10	US-09-927-483-4
43	61.6	13.1	1919	10	US-09-927-483-1
44	61.6	13.1	1919	10	US-09-927-483-2
45	59.4	12.6	77	10	US-09-974-300-4362

## ALIGNMENTS

## RESULT 1

US-09-790-988-1  
; Sequence 1, Application US/09790988  
; Patent No. US2002012687A1

GENERAL INFORMATION:

APPLICANT: SHIGENOBU, SHUJI

APPLICANT: WATANABE, HIDEKI

APPLICANT: HATTORI, MASAHIRA

APPLICANT: SAKAKI, YOSHIYUKI

TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS

FILE REFERENCE: 081356/0159

CURRENT FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: JP2000-107160

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 640681

TYPE: DNA

ORGANISM: Buchnera sp.

US-09-790-988-1

Query Match 20.2%; Score 95.2; DB 10; Length 640681;  
Best Local Similarity 69.7%; Pred. No. 2e-20;  
Matches 166; Conservative 0; Mismatches 53; Indels 19; Gaps 2;

QY 5 AAGATCCCGCTTCTTCATAGCTCCACACGAATTCCTTGAATTCATCTGTTAGACGATT 64  
Db 275585 AAAATATATATCTTTTGAAGTCCACACAAATATCTAATAAAAAATTAGA----- 275639

QY 65 GGCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGTTAGGTCGGCAGTTTCGAA 124  
Db 275640 AGGCTTGTAGTCAGATGTTAGAGCGCACCCCTGATAGGTTAGGTCGGTTCAT 275699

QY 125 TCTGCCACGACCCACCAATTTGTTGCTGCTGCTGATCCGATACGGGCCCATAGCTCAG 184  
Db 275700 TCACCTCAGGCTACCAAT-----AAAAATCATCTGGGCTATAGCTCAG 275745

QY 185 CTGGGAGAGCGCTGCTTTGTCACGAGGAGGTCAGAGTTTCATCTCTTGGCTCCA 242  
Db 275746 CTGGGAGAGCGCTGCTTGTGACGAGGTCAGCGGTTCAATCCCGCTTAGCTCCA 275803

Sequence 86, Appl  
Sequence 5, Appl  
Sequence 4361, Ap  
Sequence 4403, Ap  
Sequence 4418, Ap  
Sequence 8396, Ap  
Sequence 8438, Ap  
Sequence 8444, Ap  
Sequence 8453, Ap  
Sequence 4692, Ap  
Sequence 2687, Ap  
Sequence 96, Appl  
Sequence 869, Appl  
Sequence 550, Appl  
Sequence 102, Appl  
Sequence 4363, Ap  
Sequence 8398, Ap  
Sequence 95, Appl  
Sequence 89, Appl  
Sequence 3, Appl  
Sequence 4, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 4362, Ap









```
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1459
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1473

Query Match          19.9%; Score 93.8; DB 10; Length 255;
Best Local Similarity 72.8%; Pred. No. 8.1e-22;
Matches 139; Conservative 0; Mismatches 42; Indels 10; Gaps 1;

QY 39 TTGCTTGATTCAGTGGTGTAGACGATGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCT 98
Db 181 TTGAATGTTGTTTCATTCAAATTAATGGCCTATAGCTCAGCTGGTTAGAGCGCACCCCT 122

QY 99 GATAAGGTCAGTGGCGCCATGCTGCAATCTGCCAGACCCACCAATTTGTTGCTGCG 158
Db 121 GATAAGCGTGAGTGGTGGTTCGAGTCCACTTAGGCCCCACCAATTAATTT-----T 72

QY 159 TGATCCGATACGGGCCATGCTCAGCTGGGAGAGCGCTGCTTTGCACCGCAGAGGTCA 218
Db 71 AATACCTATTGGGGGCTTAGCTCAGCTGGGAGAGCGCTGCTTTGCACCGCAGAGGTCA 12

QY 219 GGAGTTCGATC 229
Db 11 GCGGTTTCGATC 1

RESULT 10
US-09-815-242-1473/c
; Sequence 1473, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; CURRENT APPLICATION NUMBER: US/09/815,242
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```
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; CURRENT APPLICATION NUMBER: 60/257,931
; PRIOR APPLICATION NUMBER: 60/257,931

RESULT 11
US-09-815-242-1475/c
; Sequence 1475, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; CURRENT APPLICATION NUMBER: 60/257,931
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; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1638
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; US-09-815-242-1638

Query Match          19.9%; Score 93.8; DB 10; Length 255;
Best Local Similarity 72.8%; Pred. No. 8.le-22;
Matches 139; Conservative 0; Mismatches 42; Indels 10; Gaps 1;

Qy 39 TTGCTTGAATTCACGTGGTTAGACGATTTGGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCT 98
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TTGAATGTTTTCATTCAAAATTAATGGCCCTATAGCTCAGCTGGTTAGAGCGCACGCT 122

Qy 99 GATAGGGTGAGGTCCGCGCAGTTCCGAATCTGCCAGACCCACCAATGTTGGTGTCTGCG 158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GATAAGCGTGAGGTGCGTGGTTGCTGAGTCCACTTAGGCCCCACCATTAATTT-----T 72

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QY 159 TGATCCGATACGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGCAGGAGGTCA 218

Db 71 AATACCTATTGGGGCTAGCTCAGCTGGGAGAGCGCTCTTGCACGAGAGGTCA 12  
QY 219 GGAGTTGATC 229  
Db 11 GCGGTTGATC 1

## RESULT 14

US-09-863-086-87  
; Sequence 87, Application US/09863086  
; Patent No. US20020048762A1  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
; REGION BETWEEN THE 16S A  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/863,086  
; FILING DATE: 22-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/312,520  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/412,614  
; FILING DATE: 29-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillison, Randall A  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.75USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/332-5300  
; TELEFAX: 612/332/9081  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 582 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: <Unknown>  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 87:  
US-09-863-086-87

Query Match 19.7%; Score 92.6; DB 10; Length 582;  
Best Local Similarity 74.0%; Pred. No. 3.2e-21;  
Matches 134; Conservative 0; Mismatches 39; Indels 8; Gaps 1;  
QY 65 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGGTGAGGTGGCGAGTTCGAA 124  
Db 98 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGGTGAGGTGGCGAGTTCGAA 157  
QY 125 TCTGCCAGACCCACCAATTTGGTGTGCTGATCGGATACGGGGGCATAGCTCAG 184  
Db 158 TCCAAACAGACCCACCAAGTTCTCTGAGAGG-----GAAATGGGGGTGTAGCTCAG 209  
QY 185 CTGGGAGAGCGGCTGCTTTGACGAGGAGGTTCAGAGTTCGATCCTCTTGGCTCCACC 244

Db 210 CTGGGAGAGCGGCTCTTGGTTCGAAGCAGGATGTCATCGGTTCGATCCCGTTCACCTCCACC 269  
QY 245 A 245  
Db 270 A 270

## RESULT 15

US-09-863-086-88  
; Sequence 88, Application US/09863086  
; Patent No. US20020048762A1  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
; REGION BETWEEN THE 16S A  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/863,086  
; FILING DATE: 22-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/312,520  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/412,614  
; FILING DATE: 29-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillison, Randall A  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.75USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/332-5300  
; TELEFAX: 612/332/9081  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 590 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: <Unknown>  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 88:  
US-09-863-086-88

Query Match 19.7%; Score 92.6; DB 10; Length 590;  
Best Local Similarity 74.0%; Pred. No. 3.3e-21;  
Matches 134; Conservative 0; Mismatches 39; Indels 8; Gaps 1;  
QY 65 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGGTGAGGTGGCGAGTTCGAA 124  
Db 98 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGGTGAGGTGGCGAGTTCGAA 157  
QY 125 TCTGCCAGACCCACCAATTTGGTGTGCTGATCGGATACGGGGGCATAGCTCAG 184  
Db 158 TCCAAACAGACCCACCAAGTTCTCTGAGAGG-----GAAATGGGGGTGTAGCTCAG 209  
QY 185 CTGGGAGAGCGGCTGCTTTGACGAGGAGGTTCAGAGTTCGATCCTCTTGGCTCCACC 244

Db 210 CTGGGAGAGCGCCTGCTTTGCAAGCAGGATGTCATCGGTTGATCCCGTTTCACCTCCACC 269  
QY 245 A 245  
Db 270 A 270

Search completed: February 1, 2003, 06:47:34  
Job time : 247.209 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:09:56 ; Search time 878.868 Seconds  
(without alignments)  
8679.427 Million cell updates/sec

Title: US-09-931-486-111

Perfect score: 471

Sequence: 1 ATCGAAGATCCGGCTTCTT.....CAGATTGCTGGGTATAT 471

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
c 1	266.6	56.6	507	17	BH200120	BH200120 Sm1-57J2.
c 2	264.8	56.2	629	17	BH201541	BH201541 Sm1-57P13
c 3	184.6	39.2	639	17	AO509640	AO509640 nbxb0096P
c 4	121.6	25.8	319	10	BE092111	BE092111 IL2-BT073
c 5	73.6	15.6	754	17	BH405252	BH405252 AG-ND-127
c 6	71.6	15.2	712	17	BH397037	BH397037 AG-ND-137

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

c	7	14.9	70	619	9	AA680996
c 8	63.8	13.5	63.8	6499	17	BH771024
c 9	63.2	13.4	63.2	577	17	BH819575
c 10	63	13.4	63	593	17	BH400944
c 11	63	13.4	63	760	17	BH393190
c 12	60.2	12.8	60.2	696	17	BH393241
c 13	59.6	12.7	59.6	497	13	B1544108
c 14	59.6	12.7	59.6	548	13	B1544155
c 15	58.6	12.4	58.6	287	17	BH614410
c 16	58	12.3	58	539	13	B1544086
c 17	58	12.3	58	608	17	BH375641
c 18	57.4	12.2	57.4	191	17	AZ578476
c 19	55.2	11.7	55.2	617	9	AI526132
c 20	52.4	11.1	52.4	904	17	BH159957
c 21	52	11.0	52	2149	17	AQ012191
c 22	48.2	10.2	48.2	432	13	B1941477
c 23	47.8	10.1	47.8	541	17	BH387664
c 24	47.6	10.1	47.6	612	17	AQ989869
c 25	47.4	10.1	47.4	702	17	BH586090
c 26	47.2	10.0	47.2	579	17	BH375975
c 27	47	10.0	47	938	17	AZ683938
c 28	46.6	9.9	46.6	679	13	B1263958
c 29	46	9.8	46	666	17	AQ959605
c 30	46	9.8	46	710	17	AQ967686
c 31	45.2	9.6	45.2	337	10	AW238775
c 32	45.2	9.6	45.2	381	10	AW238039
c 33	45.2	9.6	45.2	411	10	AW238064
c 34	45.2	9.6	45.2	450	12	BG272878
c 35	45.2	9.6	45.2	640	17	BH584916
c 36	45	9.6	45	759	17	BH427885
c 37	44.8	9.5	44.8	715	17	BH375497
c 38	44.4	9.4	44.4	874	17	CNS06GSM
c 39	44.2	9.4	44.2	687	17	BH570140
c 40	44.2	9.4	44.2	704	17	BH427896
c 41	44.2	9.4	44.2	727	17	BH427934
c 42	44.2	9.4	44.2	750	17	BH646171
c 43	44.2	9.4	44.2	905	17	AZ672622
c 44	44	9.3	44	197	17	BH855109
c 45	44	9.3	44	216	17	BH169234

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BH200120/c	BH200120	Sm1-57J2.TF Sm1 Schistosoma mansoni genomic clone Sm1-57J2, DNA sequence.	BH200120	BH200120.1	GI:16370164	GSS.	Schistosoma mansoni.	Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed ,N.M.	Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sm1 BAC library for gene discovery and map construction	Strigeidida; Schistosomatidae; Schistosoma.	Unpublished (2001)	Other_GSSs: Sm1-57J2.TR
							Schistosoma mansoni.					Contact: Najib M. El-Sayed
							Schistosoma mansoni.					Department of Eukaryotic Genomics
							Schistosoma mansoni.					The Institute for Genomic Research
							Schistosoma mansoni.					9712 Medical Center Dr., Rockville, MD 20850, USA
							Schistosoma mansoni.					Tel: 301 838 0200
							Schistosoma mansoni.					Fax: 301 838 0208
							Schistosoma mansoni.					Email: nelsayed@tigr.org
							Schistosoma mansoni.					lo.edu).
							Schistosoma mansoni.					Seq primer: M13 For
							Schistosoma mansoni.					Class: BAC ends.



AQ509640  
 AQ509640.1 GI:4733723  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Oryza sativa.  
 Oryza sativa.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 639)  
 Wing, R.A. and Dean, R.A.  
 A BAC End Sequencing Framework to Sequence the Rice Genome  
 Unpublished (1998)  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: twing@clemson.edu  
 Seq primer: TAATACGACTCACTATAGGG  
 Class: BAC ends  
 High quality sequence start: 86  
 High quality sequence stop: 304.  
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 source  
 1..639  
 /organism="Oryza sativa"  
 /strain="Japonica"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:4530"  
 /clone="nbxb0096p15f"  
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 /tissue\_type="leaf"  
 /lab\_host="E. coli DH10B"  
 /note="vector: pBeloBAC11; Site:1: HindIII; Site:2:  
 HindIII; Rice is one of two most popular grains in the  
 world. Half of the world population especially those  
 inhabiting highly populated areas of the humid tropics  
 and subtropics, rely on rice as their primary source of  
 carbohydrate. Monocotyledonous rice is a diploid plant  
 (2n=24) with a haploid genome equivalent of 431 Mbp  
 (Arumuganathan and Earle, 1991). The relatively small  
 genome of rice, three times larger than that of  
 Arabidopsis, makes it suitable for genomic studies. In  
 order to facilitate positional cloning, physical mapping  
 and genome sequencing of rice, we have constructed a BAC  
 library from Oryza sativa, Nipponbare variety. The  
 library contains 36,864 clones with an average insert size  
 of 128.5 Kb providing 10.9 haploid genome equivalents. The  
 deep coverage allows the isolation a particular sequence  
 with a probability of 99.9 %. Two high density filters,  
 each containing 18,432 clones (doubly spotted), represent  
 the whole library for colony screening."  
 158 a 175 c 148 g 156 t  
 BASE COUNT  
 ORIGIN  
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 Best Local Similarity 78.8%; Pred. No. 5.1e-47;  
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 QY 53 GGTAGACATTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGGTTAGGT 112  
 DB 587 GGTAGACAGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGGTTAGGT 528  
 QY 113 CGGCAGTTGGAATCTCCACAGACCCCAATTTGTTGCTGCTGCGATCCGATACGGG 172  
 DB 527 CGGCAGTTGGAATCTCCACAGACCCCAATTTGTTGCTGCTGCGATCCGATACGGG 489  
 QY 173 GCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGACGAGGAGGTGAGGTTGATCTC 232  
 DB 488 GCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGACGAGGAGGTGAGGTTGATCTC 429  
 QY 233 CTGGGCTCCACCATCTTAAACAATCGTGC-----AAAGCTCAGAAATG 275  
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Db 428 CTGGCTCCACCATCTCCACCCCTGTGTCGATAACACGATTGCTTGAAGAGCTCAGAGTG 369  
 QY 276 AATGTCG-TGGATGAACATTGATTTCTGGTCTTTGACACGAACTGTTCTTTAAATTT 334  
 ||||||| ||| ||||||||||| ||||||||||| ||||||||||| |||||||  
 Db 368 AGTGTTCGCTGGCAATCTGACTTCTGGTCTTTG-ATCAGAACTGTTCTTTAAATAAT 310  
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 QY 335 CGGATGATGATAGAGTAAGATCAATGATCTCTTTCACCTGGTGGTATCATTCAGTCAAG 394  
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 Db 309 TCGGAAGTGATAGAGT-AGACACATTCGACTGTTTTCACGGCAGTGCATGCTGCTCAAG 251  
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 QY 395 GTAAAT-TTGGAGTTCAAGCGCAATTTTCGGCG-ATGTCGCTTTCAC 443  
 ||||||| ||||||| ||| ||| ||||||||||| ||| ||||||| ||| |||||||  
 Db 250 GTAAATCTTGGCAACTCAAGCGCAAGTTTTCGGCGAAATGTCGCTTTCAC 200  
 ||||||| ||||||| ||| ||| ||||||||||| ||| ||||||| ||| |||||||  
 RESULT 4  
 BE092111 319 bp mRNA linear EST 12-JUN-2000  
 LOCUS IL2-BT0733-240400-073-G03 BT0733 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BE092111  
 ACCESSION BE092111  
 VERSION BE092111.1 GI:8482563  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 319)  
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bal, G.S., Simpson, D.H.,  
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 CONTACT: Simpson A.J.G.  
 LABORATORY of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=62-IL2-BT0733-240  
 400-073-G03&t3=2000-04-24&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 298.  
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 /db\_xref="taxon:9606"  
 /clone\_lib="BT0733"  
 /dev\_stage="Adult"  
 /note="Organ: breast; Vector: puc18; Site:1: SmaI; Site:2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (O.S. Letters Patent application No. 196  
 /716 - Ludwig Institute for Cancer Research) profiles  
 into the puc 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."  
 73 a 62 c 91 g 93 t  
 BASE COUNT  
 ORIGIN  
 Query Match 25.8%; Score 121.6; DB 10; Length 319;  
 Best Local Similarity 85.1%; Pred. No. 2.5e-27;  
 Matches 148; Conservative 0; Mismatches 24; Indels 2; Gaps 1;  
 QY 78 AGTGGTTAGACGCGACCCCTGTATAGGTTGAGTGGCAGTTCGATTCGCCAGACCC 137  
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Db 1 ACTTGTTAGAGCGCACCTTTGATAGAGGTGAGGTGCGCAGTTGGAATCTGCCGAGACCC 60
QY 138 ACCAA--TTGTGTGTGTCGTGATCCGATACGGGCGCATAGCTCAGCTGGGAGAGCG 195
Db 61 ACCAATCTGTGCGGGAAGCCTGTAGAAATACGGGCGCATAGCTCAGCTGGGAGAGCG 120
QY 196 CCGTCTTTCAGCAGGAGGTCAGGAGTTCGATCCCTCTGGCTCCACCATCTA 249
Db 121 CTGCTCTTCACGAGGAGGTCAACGGTTCGATCCCGTTGGCTCCACCATTTA 174

RESULT 5
BH405252/c
LOCUS BH405252
DEFINITION AG-ND-127K13.TR ND-TAM Anopheles gambiae genomic clone AG-ND-127K13
, DNA sequence.
ACCESSION BH405252
VERSION BH405252.1 GI:17351468
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 754)
AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 Rev
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..754
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/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-127K13"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
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Query Match 15.6%; Score 73.6; DB 17; Length 754;
Best Local Similarity 67.7%; Pred. No. 6.7e-12;
Matches 134; Conservative 0; Mismatches 59; Indels 5; Gaps 2;

QY 53 GGTAGCATTGGGTCTAGCTAGTGGTTAGAGCGCACCCCTGATAAGGGTCAGCT 112
Db 649 GGTGCTGGACTGGGTCTAGCTAGCTGGTTAGAGCACCGTCTTGTAGAGCGGGGT 590
QY 113 CGGCAGTTCGATTCGCCAGACCCACCAATTTGTTGGTGTGCTGCGATCCG ---ATA 168
Db 589 CGTTGGTTCGAGCCCAACTAGACCCACCAAGATTCCAAATGCTGTTGTCGAGGATCCCC 530
QY 169 CGGGGCGATAGCTCAGC-TGGGAGAGCGCTCTGTTTGCACGAGGAGGTCAGGATCGA 227
Db 529 CGGGGATAGCTAGCTTGGGAGAGCACCTCTGCTTTGCAAGCAGGGGGTCGTCGGTTTCA 470

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QY 228 TCCTCCTTGGCTCCACCA 245
Db 469 TCCCGTCATCCTCCACCA 452

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LOCUS BH397037
DEFINITION AG-ND-137F22.TF.1 ND-TAM Anopheles gambiae genomic clone
AG-ND-137F22, DNA sequence.
ACCESSION BH397037
VERSION BH397037.1 GI:17343253
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 712)
AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: AG-ND-137F22.TR.1
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..712
/organism="Anopheles gambiae"
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Best Local Similarity 65.1%; Pred. No. 2.8e-11;
Matches 121; Conservative 0; Mismatches 64; Indels 1; Gaps 1;

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QY 121 CGAATCTGCCAGACCCACCAATTTGTTGGTGTCTGCGTGATCCGATACGGGCGCATAGC 180
Db 612 CGAGCCCAACTAGACCCACCAATATATCCCAATATCTGTTCCGAGGATCCAGGGGATAGC 553
QY 181 TCAGCTGGGAGAGCGCTGCTTT-TGCACGACGAGGAGCTTCGATCTCTCTCTGCTT 239
Db 552 TCAGCTGGGAGAGCACATGCTTCGCCAAGCAGGGGTCTGCTGCTTCGATCCCTCATCCT 493
QY 240 CCACCA 245
Db 492 CCACCA 487

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```

RESULT 7
AA680996/c
LOCUS
DEFINITION
  AA680996 619 bp mRNA linear EST 30-DEC-1997
  SW3D9CA514SK Brugia malayi L3 molting-day 9 larva cDNA
  (SAW97MLW-Bml3d9) Brugia malayi cDNA clone SW3D9CA514 5', mRNA
  sequence.
ACCESSION
  AA680996.1 GI:2663001
VERSION
  EST.
KEYWORDS
  Brugia malayi.
SOURCE
  Brugia malayi.
ORGANISM
  Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
  Onchocercidae; Brugia.
REFERENCE
  1 (bases 1 to 619)
  Williams, S.A. and Lizotte-Waniewski, M.
  Genes expressed in day 9 post-infection, third stage larvae of
  Brugia malayi
  Unpublished (1997)
JOURNAL
  Contact: Steven A. Williams
COMMENT
  Molecular Parasitology
  Smith College Department of Biological Sciences
  Department of Biological Sciences, Clark Science Center, Smith
  College, Northampton, MA, 01063, USA
  Tel: 4135853826
  Fax: 4135853786
  Email: genome@smith.edu
  Seq primer: pBluescript SK.
  Location/Qualifiers
    1..619
    /organism="Brugia malayi"
    /db_xref="taxon:6279"
    /clone="SW3D9CA514"
    /clone_lib="Brugia malayi L3 molting-day 9 larva cDNA
    (SAW97MLW-Bml3d9)"
    /dev_stage="third stage larvae, nine days after infection"
    /lab_host="E. coli XL1-Blue MRF."
    /note="Vector: Lambda Zap II (Unizap XR); Site_1: Eco RI
    (5' end); Site_2: Xho I (3' end); Brugia malayi is a
    lymphatic filarial nematode parasite of humans. mRNA was
    prepared from third stage larvae of Brugia malayi
    isolated from the peritoneal cavity of birds nine days
    after infection. The mRNA was converted to double
    stranded cDNA using reverse transcriptase and oligo (dT)
    followed by Knaase H and DNAPol I. The library was
    constructed by Michelle Lizotte-Waniewski. The library is
    available from the Filarial Genome Project Resource
    Center: contact Dr. S.A. Williams, Clark Science Center,
    Smith College, Northampton, MA 01063 USA phone +1 413
    585-3826 fax +1 413 585-3786 email genome@smith.edu"

BASE COUNT 148 a 148 c 121 g 168 t 34 others
ORIGIN
  Query Match 14.9%; Score 70; DB 9; Length 619;
  Best Local Similarity 68.8%; Pred. No. 8.1e-11;
  Matches 130; Conservative 0; Mismatches 43; Indels 16; Gaps 2;

QY 76 TCAGTTGGTTAGAGCGACCCCTGATAGGTTGAGTGGCGAGTTTCAAGTTCGCCAGAC 135
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Db 518 TCAGTTGGTTAGAGCGACCCCTGATAGGTTGAGTGGCGAGTTTCAAGTTCACATCAGC 459
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QY 136 CCACCAATTTGTTGTTGCTGCTGATCCGA-----TACGGGGCCCATAGCT 181
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Db 458 CTACCAAAATTTGCACGGCAAAATTTAGAGAGTTTAACTACATGCTATGGGTTATAGCT 399
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QY 182 CAGCTGGGAGAGCGCTGCTTTGCA--CCGAGAGGTAGGATTCGATCCTCCTTGCT 239
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Db 398 CAGCTGGGAGAGCGCTGCTTTGCA--CCGAGAGGTAGGATTCGATCCTCCTTGCT 339
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QY 240 CCACCATCT 248
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RESULT 8
BH771024
LOCUS
DEFINITION
  BH771024 6499 bp DNA linear GSS 01-MAY-2002
  LLMGTAG746 MG1363 Random Sequence Tag Library Lactococcus lactis
  subsp. cremoris genomic, DNA sequence.
ACCESSION
  BH771024.1 GI:20373981
VERSION
  GSS.
KEYWORDS
  Lactococcus lactis subsp. cremoris.
SOURCE
  Lactococcus lactis subsp. cremoris
  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
  Lactococcus.
REFERENCE
  1 (bases 1 to 6499)
  Bolotin, A., Ehrlich, S.D. and Sorokin, A.
  Studies of genomes of dairy bacteria Lactococcus lactis
  Sci. Aliments, (2002) In press
  Contact: Sorokin A
  Genetique Microbienne
  INRA
  CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
  Tel: 33 1 34 65 25 16
  Fax: 33 1 34 65 25 21
  Email: sorokine@jouy.inra.fr
  best homologue in strain Il1403 is ywgA (78%)
  Class: shotgun
  High quality sequence start: 30
  High quality sequence stop: 6471.
  Location/Qualifiers
    1..6499
    /organism="Lactococcus lactis subsp. cremoris"
    /strain="MG1363"
    /db_xref="taxon:1359"
    /clone_lib="MG1363 Random Sequence Tag Library"
    /note="Vector: pSGM2; Site_1: SmaI; Library of
    chromosomal fragments of L.lactis strain MG1363 was
    prepared by partial AluI digestion or by sonication."

BASE COUNT 1946 a 1228 c 1683 g 1642 t
ORIGIN
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  Best Local Similarity 85.5%; Pred. No. 3.8e-08;
  Matches 71; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 170 GGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGACGAGGAGTTCAGGTTGATC 229
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Db 2165 GGGGCTTAGCTCAGCTGGGAGAGCGCTGCTTTGACGAGGAGTTCAGGTTGATC 2224
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QY 230 CTCCTTGGCTCCACCATCTAAAA 252
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RESULT 9
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LOCUS
DEFINITION
  BH819575 577 bp DNA linear GSS 20-MAY-2002
  BACP13-E14.y Pristionchus pacificus BAC ends Pristionchus
  pacificus genomic, DNA sequence.
ACCESSION
  BH819575
VERSION
  BH819575.1 GI:20993843
KEYWORDS
  GSS.
SOURCE
  Pristionchus pacificus.
  Pristionchus pacificus
  Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
  Neodiplogasteridae; Pristionchus.
REFERENCE
  1 (bases 1 to 577)
  Srinivasan, J., Sinz, W., Lanz, C., Brand, A., Nandakumar, R., Raddatz
  , G., Witte, H., Keller, H., Pires da Silva, A., Jesse, T.,
  Millare, J., de Both, M., Schuster, S.C. and Sommer, R.J.
  A BAC-based genetic linkage map of the nematode Pristionchus
  pacificus
  Unpublished (2002)
  Contact: Sommer RJ
  Evolutionary Biology

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[illegible]

Db 285 TCCAGGATAGCCACCATGAATA-----AAGGGGTATAGCTCAG 324  
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 Db 325 CTGGTAGAGCGCTGCTTTTGAAGGAGCATGTACGCGGTTCAAAATCCGCTTATCTCCAAG 384  
 Qy 245 ATCTAAAA 252  
 Db 385 TTAAAAA 392

RESULT 14  
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 LOCUS  
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 ACCESSION BI544155  
 VERSION BI544155.1 GI:19033837  
 KEYWORDS EST.  
 SOURCE Gracilaria lemaneiformis.  
 ORGANISM Gracilaria lemaneiformis.  
 Eukaryota; Rhodophyta; Florideophyceae; Gracilariiales; Gracilariaceae; Gracilaria.  
 REFERENCE 1 (bases 1 to 548)  
 AUTHORS Sun, X., Yang, G.P., Mao, Y.X. and Zhang, X.C.  
 TITLE Analysis of expressed sequence tags of a marine red alga, Gracilaria lemaneiformis  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Sun, X.; Zhang, X. C.  
 College of Marine Life Sciences  
 Ocean University of Qingdao  
 Yushan Road 5, Qingdao, 266003, Shandong, China  
 Tel: +86-0532-2032789  
 Fax: +86-0532-2032276  
 Email: xc Zhang@ouqd.edu.cn  
 PCR PRIMERS  
 FORWARD: 5' -CGTGTACCATGGTCTAGAGT-3'  
 BACKWARD: 5' -CTGATCTAGACCTGCAGGCTC-3'  
 Seq primer: 5' -CGTGTACCATGGTCTAGAGT-3'  
 POLYA=Yes.

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 /organism="Gracilaria lemaneiformis"  
 /db\_xref="taxon:2778"  
 /clone\_lib="Gracilaria lemaneiformis gametophyte cDNA library"  
 /tissue\_type="gametophyte thalli"  
 /note="Vector: pMD 18-T; site 1: EcoR V with a T hang; Wild type Gracilaria lemaneiformis were harvested from Zhanshan Bay, Qingdao (China). After rinsed with boiled seawater, younger thalli was cut and washed every 3-4 days until 1 month. Then thalli was cultivated in Provasoli medium. Total RNA was isolated from thalli of gametophyte algae, using UNIQ-10 Trizol Total RNA Preparation Kit (Sangon Inc., Shanghai, China). The cDNA was synthesized, amplified and cloned using cDNA Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector (Takara Biotechnology Co., Ltd., Dalian, China), respectively."  
 BASE COUNT 183 a 92 c 107 g 166 t  
 ORIGIN

Query Match 12.7%; Score 59.6; DB 13; Length 548;  
 Best Local Similarity 63.3%; Pred. No. 1.4e-07;  
 Matches 119; Conservative 0; Mismatches 49; Indels 20; Gaps 1;  
 Qy 65 GGGCTGTAGCTCAGTTGGTTAGCGCACCCCTGATAGGCTGAGGTGGCGAGTTCGAA 124  
 Db 81 GGGCTATTAGCTCAGTTGGTTAGCGCACCCCTGATAGGCTGAGGTGGCGAGTTCGAA 140  
 Qy 125 TCTGCCAGAGCCACCAATTTGTTGTTGCTGCTCCGTCGATCCGATACGGGGCCATAGCTCAG 184

Db 141 TCCAGGATAGCCACCATGAATA-----AAGGGGTATAGCTCAG 180  
 Qy 185 CTGGAGAGCGCTCTTTGACGAGGAGGTTCAGAGTTCGATCTCTCTGGCTCCACC 244  
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 Qy 245 ATCTAAAA 252  
 Db 241 TTAAAAA 248

RESULT 15  
 BH614410  
 LOCUS  
 DEFINITION IC22A2 Subclones from overlapping BAC clones spanning the hrp cluster of Erwinia carotovora subsp. atroseptica Pectobacterium carotovorum subsp. atrosepticum genomic, DNA sequence.  
 ACCESSION BH614410  
 VERSION BH614410.1 GI:18078210  
 KEYWORDS GSS.  
 SOURCE Pectobacterium carotovorum subsp. atrosepticum.  
 ORGANISM Pectobacterium carotovorum subsp. atrosepticum.  
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Pectobacterium.  
 REFERENCE 1 (bases 1 to 287)  
 AUTHORS Bell, K.S., Avrova, A.O., Holeva, M.C., Cardie, L., Morris, W., De Jong, W., Toth, I.K., Waugh, R., Bryan, G.J. and Birch, P.R.J.  
 TITLE Sample sequencing of a selected region of the genome of Erwinia carotovora subsp. atroseptica reveal candidate phytopathogenicity genes and allows comparison with Escherichia coli  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Bell KS  
 Scottish Crop Research Institute  
 Invergowrie, Dundee, United Kingdom, DD2 5DA  
 Email: kbell@scri.sari.ac.uk  
 Class: BAC subclone.  
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 /strain="SCRI039"  
 /db\_xref="taxon:29471"  
 /clone\_lib="Subclones from overlapping BAC clones spanning the hrp cluster of Erwinia carotovora subsp. atroseptica"  
 /note="Vector: pGEM 3zf; DNA from BAC clones Eca2B8 and Eca1C22 was nebulised and cloned into pGEM 3zf and sequenced with SP6 or T7 primers"  
 BASE COUNT 74 a 62 c 78 g 73 t  
 ORIGIN

Query Match 12.4%; Score 58.6; DB 17; Length 287;  
 Best Local Similarity 82.7%; Pred. No. 1.9e-07;  
 Matches 67; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 Qy 66 GGCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGCTGAGGTTCGCGAGTTCGAAT 125  
 Db 174 GGCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGCTGAGGTTCGCGAGTTCGAAT 233  
 Qy 126 CTGCCAGAGCCACCAATTTGT 146  
 Db 234 CCACTCAGGCGCTACCAATTT 254

Search completed: February 1, 2003, 04:21:48  
 Job time : 886.868 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:06:21 ; Search time 1070.63 Seconds  
(without alignments)  
14135.156 Million cell updates/sec

Title: US-09-931-486-112

Perfect score: 520

Sequence: 1 ATCGAAGACATCAGCTCTT.....CAGATTCCTGGGGTTATAT 520

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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GenEmbl.\*

1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pi.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rtd.\*  
36: em\_htg\_rtd.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
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40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	520	100.0	520	6	A48045	A48045 Sequence 11
2	520	100.0	520	6	AR177090	AR177090 Sequence
3	520	100.0	520	6	AX191053	AX191053 Sequence
4	438.2	84.3	707	1	PSEDRO	L28162 Pseudomonas
5	397	76.3	587	1	PSED29245	AJ279245 Pseudomonas
6	396.4	76.2	705	1	PSEDEM	L28160 Pseudomonas
7	393.2	75.6	705	1	PSEDEFN	L28161 Pseudomonas
8	351.2	67.5	702	1	PSEDEF	L28159 Pseudomonas
9	278.2	53.5	616	1	AF422492	AF422492 Unculture
10	258.4	49.7	528	1	PST390589	AJ390589 Pseudomon
11	258	49.6	528	1	PST251905	AJ251905 Pseudomon
12	252.4	48.5	529	1	PST251904	AJ251904 Pseudomon
13	252.4	48.5	529	1	PST390587	AJ390587 Pseudomon
14	249	47.9	504	6	A48046	A48046 Sequence 11
15	249	47.9	504	6	AR177091	AR177091 Sequence
16	249	47.9	504	6	AX191054	AX191054 Sequence
17	249	47.9	505	1	PST251910	AJ251910 Pseudomon
18	248.8	47.8	528	1	PST251903	AJ251903 Pseudomon
19	248.6	47.8	505	1	PST390585	AJ390585 Pseudomon
20	247.4	47.6	505	1	PST390584	AJ390584 Pseudomon
21	246.6	47.4	505	1	PST390582	AJ390582 Pseudomon
22	245.8	47.3	505	1	PST390583	AJ390583 Pseudomon
23	242.6	46.7	505	1	PST251900	AJ251900 Pseudomon
24	241.2	46.4	506	1	PST390588	AJ390588 Pseudomon
25	238.2	45.8	530	1	PST251906	AJ251906 Pseudomon
26	238.2	45.8	530	1	PST251907	AJ251907 Pseudomon
27	238	45.8	506	1	PST251908	AJ251908 Pseudomon
28	235.2	45.2	560	1	AF356514	AF356514 Pseudomon
29	234.4	43.2	529	1	PST251901	AJ251901 Pseudomon
30	224.4	43.2	529	1	PST251902	AJ251902 Pseudomon
31	222	42.7	529	1	PST390590	AJ390590 Pseudomon
32	219.8	42.3	477	1	PST390586	AJ390586 Pseudomon
33	219.8	42.3	523	1	PST390581	AJ390581 Pseudomon
34	218.2	42.0	477	1	PST251909	AJ251909 Pseudomon
35	209.4	40.3	5785	1	PSU65012	U65012 Pseudomonas
36	207.6	39.9	527	1	AF127584	AF127584 Pseudomon
37	207	39.8	521	1	AF364306	AF364306 Pseudomon
38	207	39.8	521	1	AF364307	AF364307 Pseudomon
39	205.8	39.6	526	1	AF127583	AF127583 Pseudomon
40	200.8	38.6	584	1	AF197570	AF197570 Alcanivor
41	200.8	38.6	584	1	AF197571	AF197571 Alcanivor
42	200.2	38.5	567	1	PSEKDNAA	L06304 Pseudomonas
43	200.2	38.5	567	1	PSEKDNAC	L06306 Pseudomonas
44	198	38.1	523	1	AF364308	AF364308 Pseudomon
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# ALIGNMENTS

RESULT 1  
A48045  
LOCUS A48045 Sequence 112 from Patent WO9600298.  
DEFINITION A48045  
ACCESSION A48045  
VERSION A48045.1 GI:2301907  
KEYWORDS  
SOURCE .  
ORGANISM unidentified.  
unclassified  
unclassified  
REFERENCE 1 (bases 1 to 520)  
AUTHORS Jannes G., Rossau R. and Van H.H.  
TITLE SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF  
EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY  
JOURNAL Patent: WO 9600298-A 112 04-JAN-1996;  
PAT 07-MAR-1997

Pred. No. is the number of results predicted by chance to have a

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INNOGENETICS NV (BE)
Other publication AU 2924695 9601119.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 6.4e-120;
Matches 520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
AX191053
LOCUS      Sequence 112 from Patent EP1091004.
DEFINITION
ACCESSION  AX191053
VERSION     AX191053.1 GI:15149698
KEYWORDS   .
SOURCE      unidentified.
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 520)
AUTHORS     Jannes, G., Rossau, R., and van Heuverswyn, H.
TITLE       Simultaneous detection, identification and differentiation of
            eubacterial taxa using a hybridization assay
            Patent: EP 1091004-A 112 11-APR-2001;
            INNOGENETICS N.V. (BE)
FEATURES     Location/Qualifiers
            source
            i..520
            /organism="unidentified"
            /db_xref="taxon:32644"
BASE COUNT      126 a   109 c   134 g   151 t
ORIGIN

Query Match      100.0%; Score 520; DB 6; Length 520;
Best Local Similarity 100.0%; Pred. No. 6.4e-120;
Matches 520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACATCAGCTTCTTCATTAAGTATCCACAGCAATTCCTGATTTCATAGTCGAACG 60
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QY 61 AATGCTGTAAACGCGACCCCGTGTATAGGTCCTGTAGCTCAGTTGGTTAGAGCGCACCCCTG 120
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Db 421 TTGATCTGCTCAAGGTAAATTTGTTAGTTCCTCAAGACGCAAAATTTTCGGCGAATGTCGTC 480
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QY 481 TTCACGATTGAGACAGTAACCAAGATTGCTTGGGTTATAT 520
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Db 481 TTCACGATTGAGACAGTAACCAAGATTGCTTGGGTTATAT 520
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RESULT 2
ARI177090
LOCUS      Sequence 112 from patent US 6312903.
DEFINITION
ACCESSION  ARI177090
VERSION     ARI177090.1 GI:17919445
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 520)
AUTHORS     Jannes, G., Rossau, R., and Van Heuverswyn, H.
TITLE       Simultaneous detection, identification and differentiation of
            eubacterial taxa using a hybridization assay
            Patent: US 6312903-A 112 06-NOV-2001;
            INNOGENETICS N.V. (BE)
FEATURES     Location/Qualifiers
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BASE COUNT      126 a   109 c   134 g   151 t
ORIGIN

Query Match      100.0%; Score 520; DB 6; Length 520;
Best Local Similarity 100.0%; Pred. No. 6.4e-120;
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RESULT 12
LOCUS PST251904
DEFINITION Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), trna-ile
and trna-Ala, strain AN10.
ACCESSION AJ251904
VERSION AJ251904.1 GI:9844592
KEYWORDS Internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer
RNA-ile; trna-Ala; trna-ile.
SOURCE Pseudomonas stutzeri.
ORGANISM Pseudomonas stutzeri.
REFERENCE 1 (bases 1 to 529)
AUTHORS Guasp, C., Moore, E.R., Lalucat, J. and Bannasar, A.
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
MEDLINE 20393664
PUBMED 10939670
REFERENCE 2 (bases 1 to 529)
AUTHORS Bannasar, A.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
FEATURES
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/anticodon="(pos:127..129,aa:ile)
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Query Match 48.5%; Score 252.4; DB 1; Length 529;
Best Local Similarity 73.9%; Pred. No. 9.4e-53;
Matches 396; Conservative 0; Mismatches 116; Indels 24; Gaps 5;
QY 1 ATCGAAGACATCAGCTTCTTCAAGTATCCACACGAATTGCTTGATTTCATAGTCGAACG 60
Db |||||
2 ATCGAAGACTTCAGCTTCTTCAAGTATCCACACGAATTGCTTGATTTCATAGTCGAACG 60
Db |||||
QY 61 AATGCTGTAAACCGACCCCGCTGTATA-----GGTCTGTAGCTCAGTTCAGTTCAGTTCGCA 114
Db |||||
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Db |||||
QY 115 CCCCTGATAAGGTCAGTTCGCGAGTTCAATCTGCCAGACCTACCAATTG-----166
Db |||||
122 CCCCTGATAAGGTCAGTTCGCGAGTTCAATCTGCCAGACCTACCAATTG-----181
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Db |||||
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QY 227 GAGTTCACCGGTCGATCCCGTGGCTCCACCACTCTCTCGTGTGGGTCAGTGTAA 286
Db |||||
242 GAGTTCACCGGTCGATCCCGTGGCTCCACCA-----TTATTCGCAATCGCTG 294
QY 287 AGATTTCAGAAATGATGCCGCTTCAGGTTTCTCTGTTGAGTGTGCTGATTCTCGTCTTTT 346

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Db 295 AAAGCTCAGAAATGAGTGTGCTTGGCATCCCTTTCATGTGTGAGGTATTGATTTCG 354
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Db |||||
355 TCTTGGCCGACAGTCTTCTTAAATAATTGAGTATGATGATGATGATGATGATGATGATG 414
QY 405 TTGCTTTCACATGCGCAATGATCTGCTCAAGGTAATAATTGTTAGTCTTCAAGACGCAAA 464
Db |||||
415 TCATCTTCACTGGTATTATTCAAGTCAAGGTAATAATTG-CGTGTTCTCTATGCAAAAT 473
QY 465 TTGCGGGAATGTCGCTTTCACAGTTCAGACAGTACCAAGTTCGTTGGGTTATAT 520
Db |||||
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RESULT 13
LOCUS PST390587
DEFINITION Pseudomonas stutzeri intergenic spacer, trna-ile and trna-Ala
genes, strain AER5.1.
ACCESSION AJ390587
VERSION AJ390587.1 GI:9844760
KEYWORDS IGS: intergenic spacer; transfer RNA ile; transfer RNA-Ala;
trna-Ala gene; trna-ile gene.
SOURCE Pseudomonas stutzeri.
ORGANISM Pseudomonas stutzeri.
REFERENCE 1 (bases 1 to 529)
AUTHORS Guasp, C., Moore, E.R., Lalucat, J. and Bannasar, A.
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
MEDLINE 20393664
PUBMED 10939670
REFERENCE 2 (bases 1 to 529)
AUTHORS Bannasar, A.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
FEATURES
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/strain="AER5.1"
/db_xref="taxon:316"
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trna 93. .169
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trna 201. .275
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/notes="codon recognized: GCA"
/anticodon="(pos:228..230,aa:Ala)
BASE COUNT 123 a 111 c 141 g 154 t
ORIGIN
Query Match 48.5%; Score 252.4; DB 1; Length 529;
Best Local Similarity 73.9%; Pred. No. 9.4e-53;
Matches 396; Conservative 0; Mismatches 116; Indels 24; Gaps 5;
QY 1 ATCGAAGACATCAGCTTCTTCAAGTATCCACACGAATTGCTTGATTTCATAGTCGAACG 60
Db |||||
2 ATCGAAGACTTCAGCTTCTTCAAGTATCCACACGAATTGCTTGATTTCATAGTCGAACG 61
QY 61 AATGCTGTAAACCGACCCCGCTGTATA-----GGTCTGTAGCTCAGTTCAGTTCAGTTCGCA 114
Db |||||
62 GCGATTGGGTTTCGACCCGAGAGACGAGTGGTCTGTAGCTCAGTTCAGTTCAGTTCGCA 121
Db |||||

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115 CCCTGATAGGGTGGAGTGGCGAGTCAAAATCTGCCAGAGCTACCAATTG-----166  
122 CCCTGATAGGGTGGAGTGGCGAGTGAATCTGCCAGAGCCACCAATGTCTATGGGA181  
167 CTGGTGCAGAGAAATACCGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAG226  
182 TGTGGCCGATCTGTAGATGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAG241  
227 GAGGTGAGGGTTCGATCCGCTTGGCTCCACCACTCTCTCGTGTGGCGTCAAGTAA286  
242 GAGGTGAGGGTTCGATCCGCTTGGCTCCACCA-----TTATCTCGACAATCGCTG294  
287 AGAGTTCAGAAATGATGGCGCTTCAGGTTTGTCTTGGAGTCTGATTCCTGGCTTTT346  
295 AAGCTCAGAAATGAGTGGCTTGGCATCTTGTGAGTGTGAGGTTATGATTTCTGG354  
347 GACGGTACGAAATGCTTCTTCAAGTGTGAGTGTGATGATGATGATGATGATGAT404  
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405 TTGCTTTCAGTGGCAATGATGCTGCTCAAGTAAATTTGTAGTCTTCAAGCGCAAAAT464  
415 TCATTTTCAGTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT473  
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RESULT 14  
A48046  
LOCUS A48046 504 bp DNA linear PAT 07-MAR-1997  
DEFINITION Sequence 113 from Patent WO9600298.  
ACCESSION A48046  
VERSION A48046.1 GI:2301908  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 504)  
AUTHORS James G. Rossau, R. and Van Heuvel, H.  
TITLE SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY  
JOURNAL Patent: WO 9600298-A 113 04-JAN-1996;  
COMMENT INNOGENETICS NV (BE)  
FEATURES Other publication AU 2924695 960119.  
Location/Qualifiers  
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Query Match 47.9%; Score 249; DB 6; Length 504;  
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Matches 392; Conservative 0; Mismatches 105; Indels 30; Gaps 5;

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QY 61 AATGCTGTAACGCGACCGCTGTATATA-----GGTCTGTAGCTCAGTTGGTGTAGAGCGCA 114  
DB 61 GCGATTGGGTTTATAGACCGGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTGTAGAGCGCA 120  
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DB 121 CCCCTGATAAGGGTGGAGTGGCGAGTTCGAAATCTGCCAGACCCCAATCG-----172  
QY 175 AGAAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTGAG 234  
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235 CGGTTGATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTGAGTGTAAAGAGTTCA 294  
225 CGGTTGATCCCGCTTGGCTCCACCACTCTAGTCCGCGAAAGCTCAGAAATGAGTGT 284  
295 GAAATGATCCCGCTTTCAGGTTTGTCTTGTAGTGTGATTTCTTGTGCTTTTGCACCGTA 354  
285 TTACCAGGATGAGGTTGATGCTGGGTGAACATGATTTCTGGACTTT-----GGC 338  
355 CGAAATACGTTCTTTTAAATTTGGATATGTATAGTAAGT-GACTGATTAATTTGCTTCA 413  
339 CCAGAACTGTTCTTTTAAATTTGGGTATGTATAGTAAGTACCGATGTTGCTTTCA 398  
414 CTGGCAATGATCTGCTCAAGGTAAATTTGTAGTCTTCAAGAGCGCAAAATTTTCGGGAA 473  
399 CTGGCAGCATGTGCGGTCAAGTAAATTTG-CGTGTTCTCTATGCAAAATTTTCGGGAA 457  
474 TGTGCTTCTCAGGATGAGACAGTAACAGATTGCTTGGGTATAT 520  
458 TGTGCTTCTCAGGTTATAGACAGTAACAGATTGCTTGGGTATAT 504

RESULT 15  
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LOCUS ARI77091 504 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 113 from patent US 6312903.  
ACCESSION ARI77091  
VERSION ARI77091.1 GI:17919446  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 504)  
AUTHORS James G. Rossau, R. and Van Heuvel, H.  
TITLE Simultaneous detection, identification and differentiation of eubacterial taxa using a hybridization assay  
JOURNAL Patent: US 6312903-A 113 06-NOV-2001;  
FEATURES Location/Qualifiers  
1..504  
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BASE COUNT 119 a 111 c 137 g 137 t  
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Query Match 47.9%; Score 249; DB 6; Length 504;  
Best Local Similarity 74.4%; Pred. No. 6.7e-52;  
Matches 392; Conservative 0; Mismatches 105; Indels 30; Gaps 5;

QY 1 ATCGAAGACATCAGCTTCTTCATAGTATCCACAGCAATGCTTGTGATTCATAGTCAAGC 60  
DB 1 ATCGAAGACACCGGCTTCGTCATAGTATCCACAGCAATGCTTGTGATTCATAGTCAAG 60  
QY 61 AATGCTGTAACGCGACCGCTGTATATA-----GGTCTGTAGCTCAGTTGGTGTAGAGCGCA 114  
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QY 175 AGAAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTGAG 234  
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QY 295 GAAATGATCCCGCTTGGCTTGTGCTGTTGAGTGTGATTTCTGCTTTTGCACCGGTA 354  
DB 285 TTACCAGGATGAGGTTGATGCTGGGTGAACATTTGCTTGGACTTT-----GGC 338  
QY 355 CGAAATACGTTCTTTTAAATTTGGATATGTATAGTAAGT-GACTGATTAATTTGCTTCA 413  
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Qy 414 CTGGCAATTGATCTGGTCAAGGTAAATTTCTAGTTCTCAAGACGCAAAATTTTCGGCGAA 473  
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Search completed: February 1, 2003, 03:05:06  
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GenCore version 5.1.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 19:23:36 ; Search time 123.136 Seconds  
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Title: US-09-931-486-112  
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Sequence: 1 ATCGAAGACATCAGCTTCTT.....CAGATTGCTGGGTATAT 520

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	520	100.0	520	17 AAT11843	P. pseudoalcaligenes
2	249	47.9	504	17 AAT11844	P. stutzeri LMG 23
3	193.2	37.2	499	17 AAT11845	P. alcaligenes LMG
4	178	34.2	468	17 AAT11846	P. putida LMG 2322
5	174	33.5	471	17 AAT11842	P. aeruginosa U2G
6	168.6	32.4	588	22 AAT16974	16S/23S rRNA spacer
7	129.2	24.8	640681	24 ABA92787	Buchnera sp. genom
8	113.8	21.9	470	17 AAT11898	Yersinia enterocol
9	111.2	21.4	582	12 AAQ14104	B. pertussis ATCC 1

10	110.8	21.3	1396	22 AAH55089	S. epidermidis gen
11	110.8	21.3	2839	22 AAH54998	S. epidermidis gen
12	110.8	21.3	3444	22 AAH54992	S. epidermidis gen
13	110.8	21.3	4429	22 AAH54300	S. epidermidis gen
14	109.4	21.0	400	18 AAV78022	Staphylococcus aur
15	109.4	21.0	400	18 AAV77902	Staphylococcus aur
16	109.4	21.0	1311	18 AAV77852	Staphylococcus aur
17	106.8	20.5	400	18 AAV77984	Staphylococcus aur
18	106.8	20.5	400	18 AAV77852	Staphylococcus aur
19	104.2	20.0	351	18 AAV78405	Staphylococcus aur
20	104	20.0	463	17 AAT11870	Listeria-like isol
21	101.4	19.5	475	17 AAT11869	Listeria-like isol
22	100	19.2	590	12 AAQ14105	B. bronchiseptica N
23	100	19.2	5097	20 AAQ24983	E. coli MG1655 rrn
24	97.8	18.8	5341	20 AAQ24986	E. coli MG1655 rrn
25	97.4	18.7	808	17 AAT11889	L. ivanovii CIP 78
26	97.4	18.7	808	17 AAT11890	Brucella melitensi
27	97.4	18.7	809	17 AAT11891	Brucella suis NIDO
28	96.8	18.6	5105	20 AAQ24989	Brucella abortus
29	96	18.5	243	23 AAS48781	E. coli MG1655 rrn
30	95.4	18.3	255	23 AAS48800	Staphylococcus aur
31	95.4	18.3	255	23 AAS48825	Staphylococcus aur
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33	95.4	18.3	255	23 AAS48846	Staphylococcus aur
34	95.4	18.3	255	23 AAS48854	Staphylococcus aur
35	95.4	18.3	255	23 AAS48877	Staphylococcus aur
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38	95.4	18.3	255	23 AAS48898	Staphylococcus aur
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41	95.4	18.3	343	18 AAV78492	Staphylococcus aur
42	95	18.3	496	17 AAT11866	L. monocytogenes I
43	95	18.3	1265	24 ABQ69060	Listeria monocytog
44	95	18.3	1409	24 ABQ70714	Listeria monocytog
45	95	18.3	5015	24 ABQ71078	Listeria monocytog

## ALIGNMENTS

RESULT 1  
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ID AAT11843 standard; DNA; 520 BP.  
AC AAT11843;  
XX  
XX 03-SEP-1996 (first entry)  
XX  
DE P. pseudoalcaligenes LMG 1225 16S-23S rRNA spacer region.  
XX  
KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.  
XX  
OS Pseudomonas pseudoalcaligenes.  
XX  
PN WO9600298-A1.  
XX  
XX 04-JAN-1996.  
XX  
XX 23-JUN-1995; 95WO-EP02452.  
PF  
XX 07-APR-1995; 95EP-0870032.  
PR 24-JUN-1994; 94EP-0870106.  
XX  
(INNO-) INNOGENETICS NV.  
PI Jannes G, Rossau R, Van Heuverswyn H;  
XX WPI; 1996-068882/07.  
XX  
PT Novel hybridisation assay for the detection of eubacteria - esp

PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 PS Claim 2; Fig 37; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from Pseudomonas  
 CC pseudoalcaligenes LMG 1225.  
 XX  
 SQ Sequence 520 BP; 126 A; 109 C; 134 G; 151 T; 0 other;

Query Match	100.0%;	Score 520;	DB 17;	Length 520;
Best Local Similarity	100.0%;	Pred No. 4e-157;		
Matches 520;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Qy     61  AATGCTGTAACGCGACCGCGTGTATAGTCTGTAGTCTAGTCTAGTGGTTAGAGCGCACCCCTG 120
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Qy     121  ATAAGGGTGAGGTGCGGCAGTTCAAATCTGCCAGACCTACCAATTCGTCGAGAGA 180
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Qy     181  ATACGGGCCATAGCTCAGCTGGAGAGCGCGCTGCCTTGACAGGAGGTTCAGCGGTC 240
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Db     241  GATCCCGCTTGGCTCCACCACCTCTCTCGTGTGCGGTGAGGTAAAGAGTTCAGAAATG 300

Qy     301  ATGCGCGCTCAGGTTTGTCTTGAGTGCTGATTTCTGGCTTTTGACCGGTACGAA 360
          |||
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Qy     481  TTCACGATTTCAGACAGTAACACAGATTCGTTGGGTTATAT 520
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 ID AAT11844 standard; DNA; 504 BP.  
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 AC AAT11844;  
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 CC  
 DT 03-SEP-1996 (first entry)  
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 XX  
 KW Probe: detection; identification; microorganism; amplify;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX  
 OS Pseudomonas stutzeri.  
 XX



RESULT 3  
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 ID AAT11845 standard; DNA; 499 BP.  
 XX  
 AC AAT11845;  
 XX  
 DT 03-SEP-1996 (first entry)  
 XX  
 DE P. alcaligenes LMG 1224 16S-23S rRNA spacer region.  
 XX  
 KW Probe; detection; identification; microorganism; amplify;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX  
 OS Pseudomonas alcaligenes.  
 XX  
 PN WO9600298-A1.  
 XX  
 PD 04-JAN-1996.  
 XX  
 PF 23-JUN-1995; 95WO-EP02452.  
 XX  
 PR 07-APR-1995; 95EP-0870032.  
 PR 24-JUN-1994; 94EP-0870106.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Jannes G, Rossau R, Van Heuverswyn H;  
 XX  
 DR WPI; 1996-068882/07.  
 XX  
 PT Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX  
 PS Claim 2; Fig 39; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from Pseudomonas  
 CC alcaligenes LMG 1224.  
 XX  
 SQ Sequence 499 BP; 123 A; 109 C; 130 G; 137 T; 0 other;  
 Query Match 37.2%; Score 193.2; DB 17; Length 499;  
 Best Local Similarity 72.8%; Pred. No. 7.6e-52;  
 Matches 386; Conservative 0; Mismatches 103; Indels 41; Gaps 9;  
 QY 1 ATCGACAGCATCAGCTTCTTCATAGTATCCACACGAATTGCTTGAATTCATAGTCGAACG 60  
 DB 1 ATCGAAGACTTCAGCTTCTTCATAGTATCCACACGAATTGCTTGAATTCATAGTCGAACG 60  
 QY 61 AATGCTGTAAACGCGACCGCTGTTATA-----GCTGTAGCTCAGTGTGTTAGAGCGCA 114  
 DB 61 GCGATTGGTGTAGACCGGAGAGTGAGATGGGTCTGTAGCTCAGTGTGTTAGAGCGCA 120  
 QY 115 CCCTGATAGGCTGAGGTGCGCAGTTCAAATCTGCCAGACCTACCAATTGCTTG---G 171  
 DB 121 CCCTGATAGGCTGAGGTGCGCAGTTCGAATCTGCCAGACCTACCAATTGCTGCGGAT 180  
 QY 172 TCAGAGAAGATACCGGGCCATAGCTCAGCTGGGAGAGCGCTGCCCTTGCACGAGAGGT 231  
 DB 181 GCCAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGGCAGCAGGAGGT 240  
 QY 232 CAGCGCTTCGATCCCGCTGGCTCCACCACTCTCTCGTGTGCGGTGAGTAAAGAGT 291  
 DB 241 CAGGAGTTCGATCTCTTGGCTCCACCACTCAACTCAG-----ATCGCTGAAGC 291  
 QY 292 TCAGAAATGATCGCGCTTCAGGTTTGTCTGTGTGAGTGTGCTGATTTCTGTTTGTACCG 351

DB 292 TCAGAAATGA-----ACATGGTAGTTCAATGTTGATTTCTGGTCTTT----- 334  
 QY 352 GTACGAAATCGTCTTTTAAATTTGGATATGTGATAGAGTCACTGATTAATTCGTTT 411  
 DB 335 GCGCCAGAACTGTTCTTTTAAATTTGGGTATGTGATAGAGTCACTGATTAATTCGTTT 393  
 QY 412 CACTGGCAATTGATCTGGTCAAGTAAATTTGTAGTTCTCAAGACGCAAAATTTTCGGCG 471  
 DB 394 CACTGCAGTTG--TTAATCAAGCAAAATTTG--CGAGTCAAGCCGGAATTTTCGGCG 449  
 QY 472 AATGCTGCTTCTCAGAT-TGAGACAGTAAACCAGATTCCTTTGGGTTATAT 520  
 DB 450 AATGCTGCTTCTCAGATTACGAATCTATAACCAGATTCCTTTGGGTTATAT 499  
 RESULT 4  
 AAT11846  
 ID AAT11846 standard; DNA; 468 BP.  
 XX  
 AC AAT11846;  
 XX  
 DT 03-SEP-1996 (first entry)  
 XX  
 DE P. putida LMG 2232 16S-23S rRNA spacer region.  
 XX  
 KW Probe; detection; identification; microorganism; amplify;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX  
 OS Pseudomonas putida.  
 XX  
 PN WO9600298-A1.  
 XX  
 PD 04-JAN-1996.  
 XX  
 PF 23-JUN-1995; 95WO-EP02452.  
 XX  
 PR 07-APR-1995; 95EP-0870032.  
 PR 24-JUN-1994; 94EP-0870106.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Jannes G, Rossau R, Van Heuverswyn H;  
 XX  
 DR WPI; 1996-068882/07.  
 XX  
 PT Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX  
 PS Claim 2; Fig 40; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from Pseudomonas  
 CC putida LMG 2232.  
 XX  
 SQ Sequence 468 BP; 117 A; 101 C; 117 G; 133 T; 0 other;  
 Query Match 34.2%; Score 178; DB 17; Length 468;  
 Best Local Similarity 71.1%; Pred. No. 5.8e-47;  
 Matches 371; Conservative 0; Mismatches 95; Indels 56; Gaps 8;  
 QY 1 ATCGACAGCATCAGCTTCTTCATAGTATCCACACGAATTGCTTGAATTCATAGTCGAACG 60  
 DB 1 ATCGACAGCATCAGCTTCTTCATAGTATCCACACGAATTGCTTGAATTCATAGTCGAACG 60  
 QY 61 AATGCTGTAAACGCGACCGCTGTTATAGTCTCTGTAGTGTGTTAGAGCGCACCCCTG 120

Db 61 CGATTAGGTAGCAACCTTCGAT - TGGGTCTGTAGCTCAGTGGTTAGCGCACCCCTG 119  
 QY 121 ATAGAGGTAGGTGGCGAGTTCATTAATCTGCCAGACCTACCAATTCGTTGGTCGAGAGA 180  
 Db 120 ATAGAGGTAGGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGCT----- 168  
 QY 181 ATAGGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGGCTTGCACGAGGAGTCAGGGTTC 240  
 Db 169 ----GGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGGCTTGCACGAGGAGTCAGGGTTC 224  
 QY 241 GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGCGGTGAGTGTAAAGAGTTCAGAAATG 300  
 Db 225 GATCCCGCTTGGCTCCACCACTC-----CGCTTGGCAGTTCGAAAGCTTAGAATG 277  
 QY 301 ATGCCCGCTCAGGTTTCTGTTAGTGTGCTGATTTCTGGTCTTTTACCAGGTAGGAAA 360  
 Db 278 A-----ATATTCCGCTGCAATATTGATTCTGTAACCTT-----TATCAGAA 317  
 QY 361 TCGTCTCTTAAATTTGGATATGTGATAGAGTGAAGTGAATTAATG--CTTTCACCTGTC 418  
 Db 318 TCGTCTCTTAAATTTGGATATGTGATAGAGTGAAGTGAATTAATG--CTTTCACCTGTC 377  
 QY 419 AATTGATCTGGTCAAGGTAAATTTGTAGTTCTCAAGACGCAAAATTTTCGGCGGATGTCG 478  
 Db 378 GTGTGTTTCAGGCTAAGCTAAATTTGTAGT---AATTCAAGTTCGCGGATGTTG 433  
 QY 479 TCTTCAGGATGACAGTAAACAGATTCACAGATTCGTTGGGGTTATAT 520  
 Db 434 TCTTCAC-----AGTATAACCAAGATTGCTTGGGGTTATAT 468

## RESULT 5

AAT11842  
 ID AAT11842 standard; DNA; 471 BP.

XX AAT11842;

XX 03-SEP-1996 (first entry)

DE P. aeruginosa UZG 5669 16S-23S rRNA spacer region.

XX Probe; detection; identification; microorganism; amplify;

KW 16S-23S rRNA spacer region; respiratory tract; universal;

KW species-specific; ss.

XX Pseudomonas aeruginosa.

OS WO9600298-A1.

PN 04-JAN-1996.

XX 23-JUN-1995; 95WO-EP02452.

XX 07-APR-1995; 95EP-0870032.

PR 24-JUN-1994; 94EP-0870106.

XX (INNO-) INNOGENETICS NV.

XX Jannes G, Rossau R, Van Heuverswyn H;

XX WPI; 1996-068882/07.

XX Novel hybridisation assay for the detection of eubacteria - esp

PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region

XX Claim 2; Fig 36; 248pp; English.

CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes

CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *aeruginosa* UZG 5669.

XX Sequence 471 BP; 116 A; 103 C; 120 G; 132 T; 0 other;

QY Query Match 33.5%; Score 174; DB 17; Length 471;

XX Best Local Similarity 70.6%; Pred. No. 1.1e-45;

XX Matches 373; Conservative 0; Mismatches 90; Indels 65; Gaps 8;

QY 1 ATCGAAGACATCAGCTTCTTCATAAGTATCCACACGAATTCGTTGATTCATAGTCGAACG 60

Db 1 ATCGAAGATCCCGGCTTCTTCATAAGCTCCACACGAATTCGTTGATTCATAGTCGAACG 60

QY 61 AATGCTGTAAACGCGACCCCGTGTATAGGCTCTAGCTCAGTGGTTAGAGCGCACCCCTG 120

Db 61 GAT-----TGGGTCTGTAGCTCAGTGGTTAGAGCGCACCCCTG 99

QY 121 ATAAGGTCAGGTCGCGCAGTTCAAATCTGCCAGACCTACCAATTCGTTGTCGAGAG- 179

Db 100 ATAAGGTCAGGTCGCGCAGTTCGAATCTGCCAGACCCACCAATTCGTTGTCGTCGCT 159

QY 180 -----AATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCTTGCACGAGGAGTCAG 234

Db 160 GATCCGATAGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCTTGCACGAGGAGTCAG 219

QY 235 CGGTCGATCCCGCTTGGGTCCACCACCTCTCTCGTGTGGGTGAGTGTAAAGAGTTCA 294

Db 220 GAGTTCGATCTCTTGGGTCCACCA-----TCTAAACAATCGTCGAAAGCTCA 269

QY 295 GAAATGATCCCGCTTCAGGTTTGTCTCTGTGAGTGTGATTCGTTGACCGGTA 354

Db 270 GAAATGA-----ATGTTCTGGATGAACATTCGTTGTCGCTTTT 312

QY 355 CGAAATCTGTTCTTAAATAATTTGGATATGTGATAGAGT--GACTGATTAATTCGTTTC 412

Db 313 CCAGAACTGTTCTTAAATAATTCGGGTATGTGATAGAGTAAAGTAAAGTAAATTCCTTC 372

QY 413 ACTGCCAATTCGTTCTCAAGTAAATAATTTGATTTCTCAAGACGCAAAATTTTCGGCGA 472

Db 373 ACTGGTGATCATTCGAAGTCAAGTAAATAATTTG--CGAGTTCAAGCGCGAAATTTTCGGCGA 430

QY 473 ATGTCGTCCTTCAGGATTCAGACAGTAACCAAGATTCGTTGGGGTTATAT 520

Db 431 ATGTCGTCCTTCAC-----AGTATAACCAAGATTCGTTGGGGTTATAT 471

## RESULT 6

AAI69774  
 ID AAI69774 standard; DNA; 588 BP.

XX AAI69774;

XX 13-DEC-2001 (first entry)

XX 16S/23SrRNA spacer region.

XX Bacterium detection; 16S/23SrRNA spacer region; ds.

XX *Pseudomonas putida*.

XX JP2001190279-A.

XX 17-JUL-2001.

XX 13-JAN-2000; 2000JP-0004160.

XX 13-JAN-2000; 2000JP-0004160.

XX (MITO ) MITSUBISHI JUKOGYO KK.

XX WPI; 2001-605311/69.



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PD 04-JAN-1996.
XX
XX PF 23-JUN-1995; 95WO-EP02452.
XX
XX PR 07-APR-1995; 95EP-0870032.
XX
XX PR 24-JUN-1994; 94EP-0870106.
XX
XX PA (INNO-) INNOGENETICS NV.
XX
XX PI Jannes G, Rossau R, Van Heuverswyn H;
XX
XX WPI; 1996-068882/07.
XX
XX Novel hybridisation assay for the detection of eubacteria - esp
XX Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
XX PS Claim 5; Fig 98; 248pp; English.
XX
XX CC The sequences given in AAT11889-905 represent the 16S-23S rRNA spacer
XX regions derived from various microorganisms. These sequences were
XX used in the method of the invention for the detection and identification
XX of at least one or more microorganisms. The method comprises amplifying
XX the 16S-23S rRNA spacer region and hybridising one or more probes to
XX the amplified sequence. These probes were specifically used to detect
XX microorganisms in samples originating from food. This spacer region is
XX derived from Yersinia enterocolitica strain P95.
XX
XX SQ Sequence 470 BP; 129 A; 101 C; 120 G; 120 T; 0 other;

Query Match 21.9%; Score 113.8; DB 17; Length 470;
Best Local Similarity 77.1%; Pred. No. 2.8e-26;
Matches 158; Conservative 0; Mismatches 32; Indels 15; Gaps 1;

QY 82 TTATAGGCTCTGAGTCAGTTGGTTAGAGCGCACCCCTGATAGGGTGAGGTGGCGAGTT 141
Db 72 TTATAGGCTCTGAGTCAGTTGGTTAGAGCGCACCCCTGATAGGGTGAGGTGGTGTT 131
QY 142 CAAATCTGCCAGACCTACCAATTTGCTTGGTCGAGAGAAATAC-----GG 186
Db 132 CAAGTCCACTCAGGCGCTACCACTTCTCGAAGTGGAAGGTAAGTGCACGTGACTGTATGG 191
QY 187 GGCATAGTCAGCTGGGAGAGCGCTGCTTCACGACGAGAGGTGACGCGTTCGATCCC 246
Db 192 GGCATAGTCAGCTGGGAGAGCGCTGCTTCACGACGAGAGGTGACGCGTTCGATCCC 251
QY 247 GCTTGGCTCCACACCTCTCTCGGT 271
Db 252 GCTTGGCTCCACCATATAGTCTCTGT 276

RESULT 9
AAQ14104
ID AAQ14104 standard; DNA; 582 BP.
XX
XX AC AAQ14104;
XX
XX DT 10-JAN-1992 (first entry)
XX
XX DE B.pertussis ATCC 10380 16S to 23S rRNA gene spacer region.
XX
XX KW rRNA gene; ribosomal RNA; probe; ss.
XX
XX OS Bordetella pertussis ATCC 10380.
XX
XX PN EP452596-A.
XX
XX PD 23-OCT-1991.
XX
XX PF 18-APR-1990; 90EP-0401054.
XX
XX PR 18-APR-1990; 90EP-0401054.
XX
XX PA (INNO-) INNOGENETICS NV SA.

XX Rossau R, Van Heuverswyn H;
XX WPI; 1991-311940/43.
XX Hybridisation probes for detecting non-viral microorganisms -
XX derived from spacer region between 16S and 23S rRNA genes, for
XX detecting e.g. BORDETELLA PERTUSSIS, NEISSERIA GONORRHOEA
XX
XX PS Disclosure; Fig 2; 41pp; English.
XX
XX CC This sequence is the non-coding strand of the 16S-23S rRNA gene
XX spacer region; the 5'-end is proximal to the 16S rRNA gene and the 3'-
XX end proximal to the 23S rRNA gene. A set of probes were designed
XX based on this sequence which were specific for B.pertussis. A kit
XX is provided for detection of this species using the probes.
XX
XX SQ Sequence 582 BP; 136 A; 114 C; 181 G; 148 T; 3 other;

Query Match 21.4%; Score 111.2; DB 12; Length 582;
Best Local Similarity 63.4%; Pred. No. 2.2e-25;
Matches 201; Conservative 0; Mismatches 111; Indels 5; Gaps 2;

QY 67 GTAACGCGACCGCGTTATAGTCTGCTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAAG 126
Db 79 GGAGAGAGAAAGGTTTCGCGGGTCTGCTAGCTCAGTCTGCTAGAGCAGCCGCTTGTGATAAGG 138
QY 127 GTGAGTGGCGAGTTCAATCTGCCAGACCTACCAATTTGCTTGGTCGAGAAAGATACGG 186
Db 139 CGGGGGTGGTGGTTGGAATCAACACGACCCACCAA--GGTTTCTCTGAGAGGGAATGG 196
QY 187 GGCATAGTCAGCTGGGAGAGCGCTGCTTCACGACGAGAGGTGACGCGTTCGATCCC 246
Db 197 GGGTCTAGCTCAGCTGGGAGAGCGCTGCTTTCGACAGCAGGATGTCATCGTTTCGATCCC 256
QY 247 GCTTGGCTCCACCACTCTCTCGTGTGGTGGTGAAGAGTCTTAAAGAGTTCAGAAATGATGCCG 306
Db 257 GTTCACCTCCACCAAGGCTGTCAGAGAGGATGGGTGTGNNNGAGAGCCAGAGCGGAGAG 316
QY 307 CTTCAGGTTTGCCTG---TTGAGTGTCTGATTTCTGTGCTTTTGACCGGTACGAAATCG 363
Db 317 AGCAACGTTAGTGTGCGAGTCAAGTGTAAAGCGTTTAAAGCGTTGGGTTTGGCCGACGCTATATG 376
QY 364 TTCTTTAAATAATTGGA 380
Db 377 TTCTTTAAATAATTGGA 393

RESULT 10
AAH5089
ID AAH5089 standard; DNA; 1396 BP.
XX
XX AC AAH5089;
XX
XX DT 03-SEP-2001 (first entry)
XX
XX DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4453.
XX
XX KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
XX vaccination; endocarditis; ds.
XX
XX OS Staphylococcus epidermidis.
XX
XX PN WO200134809-A2.
XX
XX PD 17-MAY-2001.
XX
XX PF 09-NOV-2000; 2000WO-US30782.
XX
XX PR 09-NOV-1999; 99US-0164258.
XX
XX PA (GLAXO) GLAXO GROUP LTD.
XX
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PI Kimmerly WJ;  
 XX WPI; 2001-316495/33.  
 DR Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,  
 XX useful for vaccinating against infections, e.g. endocarditis -  
 PT Claim 8; Page 2187-2188; 2188pp; English.  
 XX  
 CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AG81454 to AG83120, from *Staphylococcus epidermidis*.  
 CC (I) and (II) can have antibacterial activity and therefore can be used  
 CC in vaccination. The nucleic acids (I) may be used to produce the  
 CC *S. epidermidis* polypeptides (II) via the production of vectors  
 CC containing them which are used to produce hosts cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of *S. epidermidis* infections, e.g. endocarditis. AAH53971 to  
 CC AAH55090 represent specifically claimed *S. epidermidis* genomic DNA  
 CC polynucleotide sequences from the present invention. AAH55091 to  
 CC AAH55098 represent oligonucleotide sequences and primers which are used  
 CC in the exemplification of the present invention.  
 CC N.B. The present invention specifically claims all the polynucleotide  
 CC sequences given in the sequence listing of the present specification,  
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
 CC no sequences are present for SEQ ID NO:4455 to 4464.  
 XX  
 SQ Sequence 1396 BP; 410 A; 254 C; 319 G; 413 T; 0 other;  
 Query Match 21.3%; Score 110.8; DB 22; Length 1396;  
 Best Local Similarity 77.1%; Pred. No. 4.5e-25;  
 Matches 148; Conservative 0; Mismatches 42; Indels 2; Gaps 1;  
 QY 80 TGTATAGTCTGTAGCTAGTGGTTAGAGCGCACCCCTGTGATAGGCTGAGTGGCGCAG 139  
 DB 639 TTTAATGGCTTATAGCTAGCTAGCTGGTTAGAGCGCACCCCTGTGATAGGCTGAGTGGCG 698  
 QY 140 TTCAATCTGCCAGACCTACCAATTCGTTGTCGAGAGAGATACGGGGCCATAGCTCAG 199  
 DB 699 TTCGAGTCCACTTAGGCCCCACCATTCAATAATT--TAAACCTTAGGGGGCTTAGCTCAG 756  
 QY 200 CTGGGAGAGCGCTCCCTTGCACGAGGAGTGCAGCGTTCGATCCCGCTTGGCTCCACC 259  
 DB 757 CTGGGAGAGCGCTCCCTTGCACGAGGAGTGCAGCGTTCGATCCCGCTTGGCTCCACC 816  
 QY 260 ACTCTCTCTCGTGT 271  
 DB 817 ATTATATTTTGT 828  
 RESULT 11  
 AAH54998/c  
 ID AAH54998 standard; DNA; 2839 BP.  
 XX  
 AC AAH54998;  
 XX  
 XX 03-SEP-2001 (first entry)  
 XX  
 DE *S. epidermidis* genomic polynucleotide sequence SEQ ID NO:4362.  
 XX  
 KW *Staphylococcus epidermidis* SRI strain; infection; diagnosis;  
 KW vaccination; endocarditis; ds.  
 XX  
 OS *Staphylococcus epidermidis*.  
 XX  
 PN WO200134809-A2.  
 XX  
 PD 17-MAY-2001.  
 XX  
 XX 09-NOV-2000; 2000WO-US30782.  
 PF

XX 09-NOV-1999; 99US-0164258.  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX Kimmerly WJ;  
 XX WPI; 2001-316495/33.  
 XX  
 PT Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,  
 XX useful for vaccinating against infections, e.g. endocarditis -  
 XX Claim 8; Page 2102; 2188pp; English.  
 XX  
 CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AG81454 to AG83120, from *Staphylococcus epidermidis*.  
 CC (I) and (II) can have antibacterial activity and therefore can be used  
 CC in vaccination. The nucleic acids (I) may be used to produce the  
 CC *S. epidermidis* polypeptides (II) via the production of vectors  
 CC containing them which are used to produce hosts cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of *S. epidermidis* infections, e.g. endocarditis. AAH53971 to  
 CC AAH55090 represent specifically claimed *S. epidermidis* genomic DNA  
 CC polynucleotide sequences from the present invention. AAH55091 to  
 CC AAH55098 represent oligonucleotide sequences and primers which are used  
 CC in the exemplification of the present invention.  
 CC N.B. The present invention specifically claims all the polynucleotide  
 CC sequences given in the sequence listing of the present specification,  
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
 CC no sequences are present for SEQ ID NO:4455 to 4464.  
 XX  
 SQ Sequence 2839 BP; 669 A; 794 C; 562 G; 814 T; 0 other;  
 Query Match 21.3%; Score 110.8; DB 22; Length 2839;  
 Best Local Similarity 77.1%; Pred. No. 6.4e-25;  
 Matches 148; Conservative 0; Mismatches 42; Indels 2; Gaps 1;  
 QY 80 TGTATAGTCTGTAGCTAGTGGTTAGAGCGCACCCCTGTGATAGGCTGAGTGGCGCAG 139  
 DB 1831 TTTAATGGCTTATAGCTAGCTAGCTGGTTAGAGCGCACCCCTGTGATAGGCTGAGTGGCG 1772  
 QY 140 TTCAATCTGCCAGACCTACCAATTCGTTGTCGAGAGAGATACGGGGCCATAGCTCAG 199  
 DB 1771 TTCGAGTCCACTTAGGCCCCACCATTCAATAATT--TAAACCTTAGGGGGCTTAGCTCAG 1714  
 QY 200 CTGGGAGAGCGCTCCCTTGCACGAGGAGTGCAGCGTTCGATCCCGCTTGGCTCCACC 259  
 DB 1713 CTGGGAGAGCGCTCCCTTGCACGAGGAGTGCAGCGTTCGATCCCGCTTGGCTCCACC 1654  
 QY 260 ACTCTCTCTCGTGT 271  
 DB 1653 ATTATATTTTGT 1642  
 RESULT 12  
 AAH54992  
 ID AAH54992 standard; DNA; 3444 BP.  
 XX  
 AC AAH54992;  
 XX  
 XX 03-SEP-2001 (first entry)  
 XX  
 DE *S. epidermidis* genomic polynucleotide sequence SEQ ID NO:4356.  
 XX  
 KW *Staphylococcus epidermidis* SRI strain; infection; diagnosis;  
 KW vaccination; endocarditis; ds.  
 XX  
 OS *Staphylococcus epidermidis*.  
 XX

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PN WO200134809-A2.
XX 17-MAY-2001.
XX 09-NOV-2000; 2000WO-US30782.
XX 09-NOV-1999; 99US-0164258.
XX (GLAX ) GLAXO GROUP LTD.
XX Kimmerly WJ;
XX WPI; 2001-316495/33.
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis -
XX Claim 8; Page 2096-2097; 2188pp; English.
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
XX (I) and (II) can have antibacterial activity and therefore can be used
XX in vaccination. The nucleic acids (I) may be used to produce the
XX S. epidermidis polypeptides (II) via the production of vectors
XX containing them which are used to produce hosts cells which express the
XX polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX used to vaccinate subjects and to raise antibodies against the bacteria.
XX The polypeptides may also be used to assay for other inhibitors of their
XX activity and therefore identify compounds that may be used for the
XX treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
XX AAH55090 represent specifically claimed S. epidermidis genomic DNA
XX polynucleotide sequences from the present invention. AAH55091 to
XX AAH55098 represent oligonucleotide sequences and primers which are used
XX in the exemplification of the present invention.
XX N.B. The present invention specifically claims all the polynucleotide
XX sequences given in the sequence listing of the present specification,
XX however the sequence listing only goes up to SEQ ID NO:4454 so even
XX though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
XX no sequences are present for SEQ ID NO:4455 to 4464.
XX SQ Sequence 3444 BP; 1203 A; 597 C; 723 G; 921 T; 0 other;

Query Match 21.3%; Score 110.8; DB 22; Length 3444;
Best Local Similarity 77.1%; Pred. No. 7.1e-25;
Matches 148; Conservative 0; Mismatches 42; Indels 2; Gaps 1;

QY 80 TGTATAGCTCTAGCTCAGTGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTGCGGCAG 139
DB 2705 TTATAGGCGCTATAGCTCAGCTGGTTAGAGCGCACGCCCTGATAAGGGTGAGGTGCGGTG 2764
QY 140 TTCAAATCGCCAGACCTACCAATTCGTTGGTCGAGAGAAATACGGGGCCATAGCTCAG 199
DB 2765 TTCGAGTCACCTTAGGCCCCACCATTTCAATAATT--TAAACCTTAGGGGCTTAGCTCAG 2822
QY 200 CTGGAGAGCGCTGCTTTCGACGAGGAGGTACAGGTTTCGATCCGCTTGGCTCCACC 259
DB 2823 CTGGAGAGCGCTGCTTTCGACGAGGAGGTACAGGTTTCGATCCGCTTAGCTCCACC 2882
QY 260 ACTCTCTCGTGT 271
DB 2883 ATTATATTTTGT 2894

RESULT 13
AAH54300
ID AAH54300 standard; DNA; 4429 BP.
XX AC AAH54300;
XX 03-SEP-2001 (first entry)
XX DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3664.
XX
```

```
KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
XX vaccination; endocarditis; ds.
OS Staphylococcus epidermidis.
PN WO200134809-A2.
XX 17-MAY-2001.
XX 09-NOV-2000; 2000WO-US30782.
XX 09-NOV-1999; 99US-0164258.
XX (GLAX ) GLAXO GROUP LTD.
XX Kimmerly WJ;
XX WPI; 2001-316495/33.
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis -
XX Claim 8; Page 1270-1272; 2188pp; English.
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
XX (I) and (II) can have antibacterial activity and therefore can be used
XX in vaccination. The nucleic acids (I) may be used to produce the
XX S. epidermidis polypeptides (II) via the production of vectors
XX containing them which are used to produce hosts cells which express the
XX polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX used to vaccinate subjects and to raise antibodies against the bacteria.
XX The polypeptides may also be used to assay for other inhibitors of their
XX activity and therefore identify compounds that may be used for the
XX treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
XX AAH55090 represent specifically claimed S. epidermidis genomic DNA
XX polynucleotide sequences from the present invention. AAH55091 to
XX AAH55098 represent oligonucleotide sequences and primers which are used
XX in the exemplification of the present invention.
XX N.B. The present invention specifically claims all the polynucleotide
XX sequences given in the sequence listing of the present specification,
XX however the sequence listing only goes up to SEQ ID NO:4454 so even
XX though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
XX no sequences are present for SEQ ID NO:4455 to 4464.
XX SQ Sequence 4429 BP; 1327 A; 928 C; 1004 G; 1170 T; 0 other;

Query Match 21.3%; Score 110.8; DB 22; Length 4429;
Best Local Similarity 77.1%; Pred. No. 8e-25;
Matches 148; Conservative 0; Mismatches 42; Indels 2; Gaps 1;

QY 80 TGTATAGCTCTAGCTCAGTGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTGCGGCAG 139
DB 2765 TTATAGGCGCTATAGCTCAGCTGGTTAGAGCGCACGCCCTGATAAGGGTGAGGTGCGGTG 2824
QY 140 TTCAAATCGCCAGACCTACCAATTCGTTGGTCGAGAGAAATACGGGGCCATAGCTCAG 199
DB 2825 TTCGAGTCACCTTAGGCCCCACCATTTCAATAATT--TAAACCTTAGGGGCTTAGCTCAG 2882
QY 200 CTGGAGAGCGCTGCTTTCGACGAGGAGGTACAGGTTTCGATCCGCTTGGCTCCACC 259
DB 2883 CTGGAGAGCGCTGCTTTCGACGAGGAGGTACAGGTTTCGATCCGCTTAGCTCCACC 2942
QY 260 ACTCTCTCGTGT 271
DB 2943 ATTATATTTTGT 2954

RESULT 14
AAV78022
ID AAV78022 standard; DNA; 400 BP.
XX AC AAV78022;
```







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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:17:06 ; Search time 27.0349 Seconds  
(without alignments)  
5898.736 Million cell updates/sec

Title: US-09-931-486-112

Perfect score: 520

Sequence: 1 ATCGAGACATCAGCTTCTT.....CAGATTGCTTGGGTTATAT 520

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : ISSUED PATENTS-NA-\*

- 1: /cgn2.6/ptodata/1/ina/5A\_COMB.seq:\*
- 2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2.6/ptodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	520	100.0	520	3	US-08-765-332-112 Sequence 112, App
2	520	100.0	520	4	US-09-448-894-112 Sequence 112, App
3	249	47.9	504	3	US-08-765-332-113 Sequence 113, App
4	249	47.9	504	4	US-09-448-894-113 Sequence 113, App
5	193.2	37.2	499	3	US-08-765-332-114 Sequence 114, App
6	193.2	37.2	499	4	US-09-448-894-114 Sequence 114, App
7	178	34.2	468	3	US-08-765-332-115 Sequence 115, App
8	178	34.2	468	4	US-09-448-894-115 Sequence 115, App
9	174	33.5	471	3	US-08-765-332-111 Sequence 111, App
10	174	33.5	471	4	US-09-448-894-111 Sequence 111, App
11	113.8	21.9	470	3	US-08-765-332-195 Sequence 195, App
12	113.8	21.9	470	4	US-09-448-894-195 Sequence 195, App
13	111	21.3	582	1	US-08-412-614-87 Sequence 87, App
14	111	21.3	582	2	US-08-635-761-87 Sequence 87, App
15	111	21.3	582	4	US-09-312-520-87 Sequence 215, App
16	104	20.0	463	3	US-08-765-332-215 Sequence 215, App
17	104	20.0	463	4	US-09-448-894-215 Sequence 215, App
18	104	20.0	475	3	US-08-765-332-214 Sequence 214, App
19	104	20.0	475	4	US-09-448-894-214 Sequence 214, App
20	101.4	19.5	590	1	US-08-412-614-88 Sequence 88, App
21	101.4	19.5	590	2	US-08-635-761-88 Sequence 88, App
22	101.4	19.5	590	4	US-09-312-520-88 Sequence 215, App
23	97.8	18.8	363	3	US-08-765-332-119 Sequence 119, App
24	97.8	18.8	363	4	US-09-448-894-119 Sequence 119, App
25	97.4	18.7	808	3	US-08-765-332-131 Sequence 131, App
26	97.4	18.7	808	4	US-09-448-894-131 Sequence 131, App
27	97.4	18.7	808	4	US-09-448-894-131 Sequence 131, App

28 97.4 18.7 808 4 US-09-448-894-132 Sequence 132, App

29 97.4 18.7 809 3 US-08-765-332-154 Sequence 154, App

30 97.4 18.7 809 4 US-09-448-894-154 Sequence 154, App

31 95 18.3 496 3 US-08-765-332-120 Sequence 120, App

32 95 18.3 496 4 US-09-448-894-120 Sequence 120, App

33 91.6 17.6 498 3 US-08-765-332-121 Sequence 121, App

34 91.6 17.6 498 4 US-09-448-894-121 Sequence 121, App

35 91.6 17.6 603 1 US-08-412-614-85 Sequence 85, App

36 91.6 17.6 603 2 US-08-635-761-85 Sequence 85, App

37 91.6 17.6 603 4 US-09-312-520-85 Sequence 85, App

38 91.6 17.6 603 4 US-09-312-520-85 Sequence 85, App

39 91.6 17.6 603 4 US-09-312-520-85 Sequence 85, App

40 91.6 17.6 603 4 US-09-312-520-85 Sequence 85, App

41 89.2 17.2 664 1 US-08-412-614-89 Sequence 89, App

42 82.8 15.9 249 3 US-08-765-332-128 Sequence 128, App

43 82.8 15.9 249 4 US-09-448-894-128 Sequence 128, App

44 81.2 15.6 618 4 US-09-703-807-15 Sequence 15, App

45 81.2 15.6 619 4 US-09-703-807-13 Sequence 13, App

## ALIGNMENTS

RESULT 1  
US-08-765-332-112  
; Sequence 112, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 112:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 520 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-765-332-112

Query Match 100.0%; Score 520; DB 3; Length 520;  
Best Local Similarity 100.0%; Pred. No. 1.4e-162;  
Matches 520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACATCAGCTTCTTCAAGTATCCACACAAATTCGTGATTCATAGTCGAACG 60  
Db 1 ATCGAAGACATCAGCTTCTTCAAGTATCCACACAAATTCGTGATTCATAGTCGAACG 60  
QY 61 AATGCTGTAAACGGACCCCGTGTATAGTCTGTAGTCTAGTGGTTAGAGCGCACCCCTG 120  
Db 61 AATGCTGTAAACGGACCCCGTGTATAGTCTGTAGTCTAGTGGTTAGAGCGCACCCCTG 120  
QY 121 ATAAGGGTGAGTTCGGCAGTTCAAAATCTGCCAGACCTACCAATTCCTTGGTCGAGAAG 180  
Db 121 ATAAGGGTGAGTTCGGCAGTTCAAAATCTGCCAGACCTACCAATTCCTTGGTCGAGAAG 180  
QY 181 ATACGGGGCCATAGTCTAGTCTGGGAGAGCGCCTTGCACGACGAGGTTCAGCGGTTTC 240  
Db 181 ATACGGGGCCATAGTCTAGTCTGGGAGAGCGCCTTGCACGACGAGGTTCAGCGGTTTC 240  
QY 241 GATCCGCTTGGCTCCACCACCTCTCTCGTGTGGCGGTGAGTGTAAAGAGTTTCAGAAATG 300  
Db 241 GATCCGCTTGGCTCCACCACCTCTCTCGTGTGGCGGTGAGTGTAAAGAGTTTCAGAAATG 300  
QY 301 ATCCGCTTACAGTTTGTCTGCTGAGTCTGATTTCTGGTCTTTCACCGGTACGAA 360  
Db 301 ATCCGCTTACAGTTTGTCTGCTGAGTCTGATTTCTGGTCTTTCACCGGTACGAA 360  
QY 361 TCGTCTTTAAATTTGGATATGTAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420  
Db 361 TCGTCTTTAAATTTGGATATGTAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420  
QY 421 TTGATCTGCTCAAGTAAATTTGATTTCTCAAGACGCAATTTTCGGCGAATTCGCTC 480  
Db 421 TTGATCTGCTCAAGTAAATTTGATTTCTCAAGACGCAATTTTCGGCGAATTCGCTC 480  
QY 481 TTCAGATTGAGACAGTAAACAGATTTCGTTGGGTTATAT 520  
Db 481 TTCAGATTGAGACAGTAAACAGATTTCGTTGGGTTATAT 520

## RESULT 2

US-09-448-894-112

; Sequence 112, Application US/09448894

; Patent No. 6312903

; GENERAL INFORMATION:

; APPLICANT: JANNES, GEERT

; ~~ROSEN, KUDI~~

; VAN HEUVERSWYN, HUGO

; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION

; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A

; HYBRIDIZATION ASSAY

; NUMBER OF SEQUENCES: 216

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON &amp; VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/09/448,894

; APPLICATION NUMBER: 6312903-1999

; FILING DATE: 29-NO. 6312903-1999

; CLASSIFICATION: <Unknown>  
; 07-APR-1995  
; 24-JUN-1994

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/765,332

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: EP 95870032.0

FILING DATE: 07-APR-1995

APPLICATION NUMBER: EP 94870106.5

FILING DATE: 24-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 1487-14

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4091

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 520 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 112:

US-09-448-894-112

Query Match 100.0%; Score 520; DB 4; Length 520;

Best Local Similarity 100.0%; Pred. No. 1.4e-162;

Matches 520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACATCAGCTTCTTCAAGTATCCACACAAATTCGTGATTCATAGTCGAACG 60  
Db 1 ATCGAAGACATCAGCTTCTTCAAGTATCCACACAAATTCGTGATTCATAGTCGAACG 60  
QY 61 AATGCTGTAAACGGACCCCGTGTATAGTCTGTAGTCTAGTGGTTAGAGCGCACCCCTG 120  
Db 61 AATGCTGTAAACGGACCCCGTGTATAGTCTGTAGTCTAGTGGTTAGAGCGCACCCCTG 120  
QY 121 ATAAGGGTGAGTTCGGCAGTTCAAAATCTGCCAGACCTACCAATTCCTTGGTCGAGAAG 180  
Db 121 ATAAGGGTGAGTTCGGCAGTTCAAAATCTGCCAGACCTACCAATTCCTTGGTCGAGAAG 180  
QY 181 ATACGGGGCCATAGTCTAGTCTGGGAGAGCGCCTTGCACGACGAGGTTCAGCGGTTTC 240  
Db 181 ATACGGGGCCATAGTCTAGTCTGGGAGAGCGCCTTGCACGACGAGGTTCAGCGGTTTC 240  
QY 241 GATCCGCTTGGCTCCACCACCTCTCTCGTGTGGCGGTGAGTGTAAAGAGTTTCAGAAATG 300  
Db 241 GATCCGCTTGGCTCCACCACCTCTCTCGTGTGGCGGTGAGTGTAAAGAGTTTCAGAAATG 300  
QY 301 ATCCGCTTACAGTTTGTCTGCTGAGTCTGATTTCTGGTCTTTCACCGGTACGAA 360  
Db 301 ATCCGCTTACAGTTTGTCTGCTGAGTCTGATTTCTGGTCTTTCACCGGTACGAA 360  
QY 361 TCGTCTTTAAATTTGGATATGTAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420  
Db 361 TCGTCTTTAAATTTGGATATGTAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420  
QY 421 TTGATCTGCTCAAGTAAATTTGATTTCTCAAGACGCAATTTTCGGCGAATTCGCTC 480  
Db 421 TTGATCTGCTCAAGTAAATTTGATTTCTCAAGACGCAATTTTCGGCGAATTCGCTC 480  
QY 481 TTCAGATTGAGACAGTAAACAGATTTCGTTGGGTTATAT 520  
Db 481 TTCAGATTGAGACAGTAAACAGATTTCGTTGGGTTATAT 520

## RESULT 3

US-08-765-332-113

; Sequence 113, Application US/08765332





ROSSAU, RUDI  
VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-Nov-6312903-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 114:  
US-09-448-894-114  
Query Match 37.2%; Score 193.2; DB 4; Length 499;  
Best Local Similarity 72.8%; Pred. No. 2.3e-54;  
Matches 386; Conservative 0; Mismatches 103; Indels 41; Gaps 9;  
QY 1 ATCGAAGACATCAGCTTCTTCATAGTATCCACACGAATGCTTGATTCATAGTCGAAGC 60  
DB 1 ATCGAAGACTCAGCTTCTTCATAGTATCCACACGAATGCTTGATTCATAGTCGAAGC 60  
QY 61 ATGCTGTACAGGACCGGCGGTGTATA-----GGTCTAGCTCAGTGGTTAGACGCGA 114  
DB 61 GCGATTGGGTTGAGACCGGAGAGTGCAGATTGGGCTGTAGCTCAGTGGTTAGACGCGA 120  
QY 115 CCCCTATAGGTTGAGTGGCGAGTTCAAATCTGCCAGACCTACCAATGCTTG--G 171  
DB 121 CCCCTGATAGGTTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATGTCGGGATG 180  
QY 172 TCAGAGAATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGT 231  
DB 181 GCGAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGT 240  
QY 232 CAGCGGTTGATCCCGCTTGGCTCCACCACTCTCTCGTGTGCGGTGAGTGTAAAGAGT 291  
DB 241 CAGGAGTTCGATCTCTTGGCTCCACCACTCAACTCAGC-----ATCGCTGAAGC 291

QY 292 TCAGAAATGATGCGCTTCAGGTTTCTGCTGCTGAGTCTGCTGATTTCTGCTTTGACCG 351  
DB 292 TCAGAAATGA-----ACATGGTAGTTCATGTTGATTTCTGCTCTTT----- 334  
QY 352 GTAGGAAATCGTTCTTTTAAATAATTTGATATGATAGAGTGAAGTGAATTAATTCGTTT 411  
DB 335 GCGCAGAACTGTTCTTTTAAATAATTTGGTATGATAGAACTGACTAACACGCTG-TTT 393  
QY 412 CACTGGCAATGATGCTGCTCAAGGTAAATAATTTGATAGTTCACAGACGCAAAATTTTCGCG 471  
DB 394 CACTGCACGTTG--TTAATCAAGGCANAATTG--CGAGTTCAAGCGGAATTTTCGCG 449  
QY 472 AATGTCGCTTTCACGAT--TGACACAGATTAACACAGATTGCTTGGGGTTATAT 520  
DB 450 AATGTCGCTTTCACGAT--TTAATCAAGGCANAATTG--CGAGTTCAAGCGGAATTTTCGCG 499  
RESULT 7  
US-08-765-332-115  
; Sequence 115, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-765-332-115

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Query Match      34.2%  Score 178;  DB 3;  Length 468;
Best Local Similarity 71.1%;  Pred. No. 2.4e-49;
Matches 371;  Conservative 0;  Mismatches 95;  Indels 56;  Gaps 8;

QY 1 ATCGAGACATCAGCTTCTTCATAGTATCCACAGCAATTCCTGATTCAATAGTCAAGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATCGAGACATCAGCTTCTTCATAGTATCCACAGCAATTCCTGATTCAATAGTCAAGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 AATGCTGTAAAGCGGCGGCTGTATAGTCTGTAGCTCAGTGTGTAGAGCGCACCCCTG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CGATTAGTTAGCAACCTTCGAT-TGGGCTGTAGCTCAGTGTGTAGAGCGCACCCCTG 119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 ATAAGGTTAGGTCGGCAGTTCAATCTGCCAGACCTACCAATTCCTGTCGAGAAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 ATAAGGTTAGGTCGGCAGTTCAATCTGCCAGACCTACCAATTCCTGTCGAGAAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 ATACGGGCCATAGCTCAGCTGGGAGAGCGCTGCTGCACGAGGAGTCAGCGGTC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 169 ----GGGCCATAGCTCAGCTGGGAGAGCGCTGCTGCACGAGGAGTCAGCGGTC 224
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 241 GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTCAGTGTAAAGAGTTCAAGAAATG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 225 GATCCCGCTTGGCTCCACCACTCTCTCGTGTGGGTCAGTGTAAAGAGTTCAAGAAATG 277
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 301 ATCCCGCTTCCAGGTTTCTCTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 278 A-----ATATTCGCGTGAATATTTGATTTCTGAACCT-----TATCAGAA 317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 361 TCCTTCTTTAAAAATTTGGATATGTATAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 418
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 318 TCCTTCTTTAAAAATTTGGATATGTATAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 419 AATTGATCTGGTCAAGTAAATTTGTAGTCTCAAGACCGCAAAATTTTCGCGCAATGTCG 478
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 378 GTGTGTTCAAGCTAAGTAAATTTGTAGTCTCAAGACCGCAAAATTTTCGCGCAATGTCG 433
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 479 TCTTCAGGATTGAGACAGTAACCAAGATTGCTTGGGTTATAT 520
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Db 434 TCTTCAC-----AGTATACCAAGATTGCTTGGGTTATAT 468
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RESULT 9
US-09-448-894-115
; Sequence 115, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
```

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US-09-448-894-115
; Sequence 115, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO

TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
HYBRIDIZATION ASSAY

NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,894
FILING DATE: 29-No. 6312903-1999
CLASSIFICATION: <Unknown>
07-APR-1995
24-JUN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,332
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Mon Feb 3 16:49:00 2003

us-09-931-486-112.rni

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APPLICATION NUMBER: 08/765,332
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95870032.0
FILING DATE: 07-APR-1995
APPLICATION NUMBER: EP 94870106.5
FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 195:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 195:
US-09-448-894-195

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Query Match 21.9%; Score 113.8; DB 4; Length 470;  
Best Local Similarity 77.1%; Pred. No. 4.4e-28;  
Matches 158; Conservative 0; Mismatches 32; Indels 15; Gaps 1;

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RESULT 13
US-08-412-614-87
; Sequence 87, Application US/08412614
; Patent No. 5536638
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudi
; APPLICANT: Van Heuverswyn, Hugo
; TITLE OF INVENTION: Hybridization Probes Derived from the
; TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the
; TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5536638west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-4131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity
; COMPUTER: IBM PC compatible (Compaq Deskpro 286e)
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,614
; FILING DATE:
; CLASSIFICATION: 435
;

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PRIOR APPLICATION DATA: 07/965.394  
APPLICATION NUMBER: 17-DEC-1992  
FILING DATE: 17-DEC-1992  
APPLICATION NUMBER: PCT/EP91/00743  
FILING DATE: 18-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB/90901054.3  
FILING DATE: 18-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75-USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 582 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bordetella pertussis  
STRAIN: ATCC 10380  
US-08-412-614-87

Query Match 21.3%; Score 111; DB 1; Length 582;  
Best Local Similarity 63.8%; Pred. No. 4.le-27;  
Matches 199; Conservative 0; Mismatches 108; Indels 5; Gaps 2;

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RESULT 14
US-08-635-761-87
; Sequence 87, Application US/08635761
; Patent No. 5945382
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: HYBRIDIZATION
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSSE: Merchant, Gould, Smith
; STREET: 3100 No. 5945282 West C
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402

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RESULT 14
US-08-635-761-87
; Sequence 87, Application US/08635761
; Patent No. 5945282
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 5945282west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402

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**CORRESPONDENCE ADDRESS:**

Matches	199;	Conservative	0;	Mismatches	108
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Search completed: February 1, 2003, 04:24:14  
Job time : 29.0349 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 03:05:22 : Search time 28.9358 Seconds  
(without alignments)  
8073.649 Million cell updates/sec

Title: US-09-931-486-112

Perfect score: 520

Sequence: 1 ATCCGAACATCAGCTCTT.....CAGATTGCTGGGGTTATAT 520

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_NA:

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	129.2	24.8	640681	10	US-09-790-988-1
2	111	21.3	582	10	Sequence 87, Appl
3	101.4	19.5	590	10	Sequence 88, Appl
C 4	96	18.5	243	10	Sequence 1358, Ap
C 5	95.4	18.3	255	10	Sequence 1377, Ap
C 6	95.4	18.3	255	10	Sequence 1402, Ap
C 7	95.4	18.3	255	10	Sequence 1415, Ap
C 8	95.4	18.3	255	10	Sequence 1423, Ap
C 9	95.4	18.3	255	10	Sequence 1431, Ap
C 10	95.4	18.3	255	10	Sequence 1434, Ap
C 11	95.4	18.3	255	10	Sequence 1459, Ap
C 12	95.4	18.3	255	10	Sequence 1473, Ap
C 13	95.4	18.3	255	10	Sequence 1475, Ap
C 14	95.4	18.3	255	10	Sequence 1483, Ap
C 15	95.4	18.3	255	10	Sequence 1638, Ap
C 16	91.6	17.6	603	10	Sequence 85, Appl
17	91.6	17.6	603	10	Sequence 86, Appl
18	84.2	16.2	3309400	9	Sequence 1, Appl
19	80.8	15.5	549	10	Sequence 92, Appl

20	80	15.4	498	10	US-09-863-086-90	Sequence 90, Appl
21	74	14.2	2336	10	US-09-842-552-102	Sequence 102, Appl
22	72.4	13.9	654	10	US-09-863-086-89	Sequence 89, Appl
C 23	72.4	13.9	1069	10	US-09-070-927A-869	Sequence 869, Appl
C 24	72	13.8	495	10	US-09-815-242-2687	Sequence 2687, Ap
C 25	72	13.8	495	10	US-09-815-242-2691	Sequence 2691, Ap
26	71.2	13.7	76	10	US-09-974-300-4361	Sequence 4361, Ap
27	71.2	13.7	76	10	US-09-974-300-4403	Sequence 4403, Ap
28	71.2	13.7	76	10	US-09-974-300-4409	Sequence 4409, Ap
29	71.2	13.7	76	10	US-09-974-300-4418	Sequence 4418, Ap
30	71.2	13.7	76	10	US-09-974-300-8396	Sequence 8396, Ap
31	71.2	13.7	76	10	US-09-974-300-8438	Sequence 8438, Ap
32	71.2	13.7	76	10	US-09-974-300-8444	Sequence 8444, Ap
33	71.2	13.7	76	10	US-09-974-300-8453	Sequence 8453, Ap
C 34	71.2	13.7	2997	10	US-09-815-242-4692	Sequence 4692, Ap
C 35	69.6	13.4	9797	10	US-09-070-927A-550	Sequence 550, Appl
36	69.2	13.3	74	10	US-09-974-300-4363	Sequence 4363, Ap
37	69.2	13.3	76	10	US-09-974-300-8398	Sequence 8398, Ap
38	68.2	13.1	246	10	US-09-863-086-95	Sequence 95, Appl
39	68.2	13.1	279	10	US-09-863-086-96	Sequence 96, Appl
40	66.8	12.8	836	9	US-09-894-467-5	Sequence 5, Appl
41	64.6	12.4	1883	10	US-09-927-483-3	Sequence 3, Appl
C 42	64.6	12.4	1883	10	US-09-927-483-4	Sequence 4, Appl
43	64.2	12.3	108	12	US-10-046-722-9	Sequence 9, Appl
C 44	63.2	12.2	213	10	US-09-815-242-1374	Sequence 1374, Ap
C 45	63.2	12.2	213	10	US-09-815-242-1375	Sequence 1375, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-790-988-1  
; Sequence 1, Application US/09790988  
; Patent No. US20020127687A1  
; GENERAL INFORMATION:  
; APPLICANT: SHIGENOBU, SHUJI  
; APPLICANT: WATANABE, HIDEMI  
; APPLICANT: HATTORI, MASAHIRO  
; APPLICANT: SAKAKI, YOSHIYUKI  
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
; FILE REFERENCE: 081356/0159  
; CURRENT APPLICATION NUMBER: US/09/790,988  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: JP2000-107160  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 640681  
; TYPE: DNA  
; ORGANISM: Buchnera sp.  
US-09-790-988-1

Query Match 24.8%; Score 129.2; DB 10; Length 640681;  
Best Local Similarity 73.4%; Pred. No. 1.7e-30;  
Matches 182; Conservative 0; Mismatches 58; Indels 8; Gaps 1;  
QY 86 AGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGCGGAGTTCAAA 145  
DB 275640 AGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGCGGAGTTCAAT 275699  
QY 146 TGTGCCCCAGACCTACCAATTTGGTTCGAGAGAAATACGGGGCCCATAGCTCAGCTGGGA 205  
DB 275700 TCCACTAGCGCTACCAA-----TAAAAAATCATCTGGGGCTATAGCTCAGCTGGGA 275751  
QY 206 GAGCGCTCCCTTGACCGCAGGAGTTCAGTCCCGTGGCTCCACCACTC 265  
DB 275752 GAGCGCTCCCTTGACCGCAGGAGTTCAGTCCCGTGGCTCCCAAAATCT 275811  
QY 266 TCGTGTTCGGTGGTGTGTTAAAGAGTTCAGAAATGATCGCGTTCAGTTTGTCTCTGTTG 325  
DB 275812 TTTTAACTTAACTTTTAAAACTTCAAAATCAGTCAGTCTTAACTTAACTTAACTTAACTT 275871

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QY 326 AGTGCTGA 333
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Db 275872 ATTCTTA 275879

RESULT 2
US-09-863-086-87
; Sequence 87, Application US/09863086
; Patent No. US20020048762A1
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER
; REGION BETWEEN THE 16S A
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,086
; FILING DATE: 22-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/312,520
; FILING DATE: <Unknown>
; NAME: Hillson, Randall A
; REGISTRATION NUMBER: 31,838
; REFERENCE/DOCKET NUMBER: 8076.75USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-09-863-086-87

Query Match 21.3%; Score 111; DB 10; Length 582;
Best Local Similarity 63.8%; Pred. No. 3e-26;
Matches 199; Conservative 0; Mismatches 108; Indels 5; Gaps 2;

QY 72 GGCACCCGTTATAGGTCGTAGCTCAGTTCAGTTGGTTAGAGCGCACCCCTGATAGGGTGAG 131
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Db 84 GAGAAAGTTTCGCGGTCGTAGCTCAGTCGTTAGAGCACCGTCTTGATAGGCGGGG 143

QY 132 GTCGGCAGTTCRAATCTGCCACCTACCAATTCGTTGTCGAGAGAATACGGGCGCA 191
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Db 144 GTCGTTGGTTCGAATCCAAACACACCCACCAA--GGTTTCCTGAGAGGAAATGGGGGTG 201

QY 192 TAGCTCAGCTGGGAGAGCGCCTGCCTTGACGAGGAGGTTCAGCGGTTTCGATCCCGCTTG 251
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Db 202 TAGCTCAGCTGGGAGAGCGCCTGCTTTGCAAGCAGGATGTCATCGCTTCGATCCCGCTTCA 261

QY 252 GCTCCACCACCTCTCTCTGTTGCGGTGAGTTTAAAGAGTTTCAAGAAATGATGCCGCTTCA 311
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Db 262 CTTCCACCAAAAGCCTGTCCAGAGGATGGGTGTGNNNGAGACCAGGAAGCGAGAGACAA 321

QY 312 GGTTCCTCCTG---TTGAGTGCCTGATTTCTGGTCTCTTTTGACCGGTACGAAATCGTTCTT 368
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Db 322 CGTTAGTGTCTGCGAGTCAGTGTAAAGCGTTGGGTTTGGCCGACAGCTATATATGTTCTT 381

QY 369 TAAATAATTTGGA 380
| | | | |
Db 382 TAACAATTTGGA 393

RESULT 3
US-09-863-086-88
; Sequence 88, Application US/09863086
; Patent No. US20020048762A1
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER
; REGION BETWEEN THE 16S A
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,086
; FILING DATE: 22-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/312,520
; FILING DATE: <Unknown>
; NAME: Hillson, Randall A
; REGISTRATION NUMBER: 31,838
; REFERENCE/DOCKET NUMBER: 8076.75USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 590 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-09-863-086-88

Query Match 19.5%; Score 101.4; DB 10; Length 590;
Best Local Similarity 74.6%; Pred. No. 4e-23;
Matches 141; Conservative 0; Mismatches 46; Indels 2; Gaps 1;

QY 72 GGCACCCGTTATAGGTCGTAGCTCAGTTCAGTTGGTTAGAGCGCACCCCTGATAGGGTGAG 131
| | | | |
Db 84 GAGAAAGTTTCGCGGTCGTAGCTCAGTCGTTAGAGCACCGTCTTGATAGGCGGGG 143
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; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1402  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1402

Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;  
  
QY 82 TTATAGTCTGTAGCTAGCTAGCTAGCGCCACCCCTGATAGGTTAGGTCGGCAGTT 141  
Db 159 TAATGGCCCTATAGCTAGCTAGCTAGCGCCACCCCTGATAGGTTAGGTCGGTGGTT 100  
  
QY 142 CAAATCTGCCAGACCTACCAATTTGTTGTCGAGAGAAATACGGGCCCATAGCTCAGCT 201  
Db 99 CGAGTCACCTTAGCGCCACCATTAATTT---AATACCTATTGGGGCTTAGCTCAGCT 44  
  
QY 202 GGGAGAGCGCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 244  
Db 43 GGGAGAGCGCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 1

RESULT 7  
US-09-815-242-1415/c  
; Sequence 1415, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1402  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1402

; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1415  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1415  
  
Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;  
  
QY 82 TTATAGTCTGTAGCTAGCTAGCTAGCGCCACCCCTGATAGGTTAGGTCGGCAGTT 141  
Db 159 TAATGGCCCTATAGCTAGCTAGCTAGCGCCACCCCTGATAGGTTAGGTCGGTGGTT 100  
  
QY 142 CAAATCTGCCAGACCTACCAATTTGTTGTCGAGAGAAATACGGGCCCATAGCTCAGCT 201  
Db 99 CGAGTCACCTTAGCGCCACCATTAATTT---AATACCTATTGGGGCTTAGCTCAGCT 44  
  
QY 202 GGGAGAGCGCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 244  
Db 43 GGGAGAGCGCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 1

RESULT 8  
US-09-815-242-1423/c  
; Sequence 1423, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1423  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1423

Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;  
  
QY 82 TTATAGTCTGTAGCTAGCTAGCTAGCGCCACCCCTGATAGGTTAGGTCGGCAGTT 141  
Db 159 TAATGGCCCTATAGCTAGCTAGCTAGCGCCACCCCTGATAGGTTAGGTCGGTGGTT 100

Db 159 TAATGGCCCTAGCTAGCTGGTTAGAGCGCACGCCCTGATAAGCGTGAGGTCGGTGGTT 100  
QY 142 CAATCTGCCAGACCTACCAATTGCTGGTCGAGAGAAATACGGGCCATAGCTCAGCT 201  
Db 99 CGAGTCCACTTAGGCCACCAATTAATTT----AATACCTATTGGGGGCTTAGCTCAGCT 44  
QY 202 GGGAGAGCGCCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 244  
Db 43 GGGAGAGCGCCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 1

## RESULT 9

US-09-815-242-1431/c  
; Sequence 1431, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1431  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus

US-09-815-242-1431  
Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;  
QY 82 TTATAGGCTGTAGCTAGCTGGTTAGAGCGCACGCCCTGATAAGGTCGAGGTCGGCAGTT 141  
Db 159 TAATGGCCCTAGCTAGCTGGTTAGAGCGCACGCCCTGATAAGGTCGAGGTCGGTGGTT 100  
QY 142 CAATCTGCCAGACCTACCAATTGCTGGTCGAGAGAAATACGGGCCATAGCTCAGCT 201  
Db 99 CGAGTCCACTTAGGCCACCAATTAATTT----AATACCTATTGGGGGCTTAGCTCAGCT 44  
QY 202 GGGAGAGCGCCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 244  
Db 43 GGGAGAGCGCCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 1

## RESULT 10

US-09-815-242-1454/c  
; Sequence 1454, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1454  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus

US-09-815-242-1454  
Query Match 18.3%; Score 95.4; DB 10; Length 255;  
Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;  
QY 82 TTATAGGCTGTAGCTAGCTGGTTAGAGCGCACGCCCTGATAAGGTCGAGGTCGGCAGTT 141  
Db 159 TAATGGCCCTAGCTAGCTGGTTAGAGCGCACGCCCTGATAAGGTCGAGGTCGGTGGTT 100  
QY 142 CAATCTGCCAGACCTACCAATTGCTGGTCGAGAGAAATACGGGCCATAGCTCAGCT 201  
Db 99 CGAGTCCACTTAGGCCACCAATTAATTT----AATACCTATTGGGGGCTTAGCTCAGCT 44  
QY 202 GGGAGAGCGCCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 244  
Db 43 GGGAGAGCGCCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 1

Query Match 18.3%; Score 95.4; DB 10; Length 255;

Best Local Similarity 78.5%; Pred. No. 2.3e-21;  
Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;

QY 82 TTATAGGCTGTAGCTAGCTGGTTAGAGCGCACGCCCTGATAAGGTCGAGGTCGGCAGTT 141  
Db 159 TAATGGCCCTAGCTAGCTGGTTAGAGCGCACGCCCTGATAAGGTCGAGGTCGGTGGTT 100  
QY 142 CAATCTGCCAGACCTACCAATTGCTGGTCGAGAGAAATACGGGCCATAGCTCAGCT 201  
Db 99 CGAGTCCACTTAGGCCACCAATTAATTT----AATACCTATTGGGGGCTTAGCTCAGCT 44  
QY 202 GGGAGAGCGCCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 244  
Db 43 GGGAGAGCGCCTGCTTGCACGACGAGGTCAGCGGTTTCGATC 1

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; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1459
;   LENGTH: 255
;   TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1459

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	Query Match	18.3%	Score 95.4;	DB 10;	Length 255;
	Best Local Similarity	78.5%;	Presd. No. 2.3e-21;		
	Matches 128;	Conservative 0;	Mismatches 31;	Indels 4;	Gaps 1;
Qy	82	TTATAGTCTGTAGCTCAGTTGGTTAGAGCCACCCCTGTATAGGTTAGGTCGCGCAGTT	141		
Db	159	TAAATGGGCGCTATAGCTCAGCTGGTTAGAGCCACCGCTGTATAGCGTTCAGTCGGTGGTT	100		
Qy	142	CAAAATCTGCCAGACCTTACCAATTCGTTGGTCGAGAGAAATACGGGGCCATAGCTCAGCT	201		
Db	99	CGAGTCACATTAGGCCACCATTAAATTT----	AATACCTAATTTGGGGCTTAGCTCAGCT	44	
Qy	202	GGGAGAGCGCTGCTTGCACGACGAGAGGTACGGGTTTCGATC	244		
Db	43	GGGAGAGCGCTGCTTGTGCACGACGAGAGGTACGGGTTTCGATC	1		

```

RESULT 12
US-09-815-242-1473/c
; Sequence 1473, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1473
; LENGTH: 255
; TYPE: DNA

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	Query Match	18.3%	Score 95.4;	DB 10;	Length 255;
	Best Local Similarity	78.5%;	Pred. No. 2.3e-21;		
	Matches 128;	Conservative 0;	Mismatches 31;	Indels 4;	Gaps 1;
Qy	82	TTATAGGTCTCTAGCTCAGTTGGTTAGAGCCACCCCTGATAAGGGTGTAGCTCGCAGTT	141		
Db	159	TAAATGGGCGCTATAGCTCAGCTGGTTAGAGCCACGCCCTGATAAGCGTGTAGCTCGGTGGTT	100		
Qy	142	CAAAATCTGCCAGACCTTACCATAATTCCTTGGTCGAGAGAATAACGGGGCCATAGCTTCAGCT	201		
Db	99	CGAGTCCACTTATGGCCCCACCAATTAATTT-----AATACCTATTGGGGGCTTAGCTCAGCT	44		
Qy	202	GGGAGAGCGGCTGCCTTGCACGCAGGAGGCTCAGGGGTTTCGATC	244		



Db 43 GGGAGAGCGCTGCTTTGCACGAGAGGTCAGCGGTTTCGATC 1  
|||||

## RESULT 14

US-09-815-242-1544/c  
; Sequence 1544, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.

; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1544

; LENGTH: 255

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-09-815-242-1544

Query Match 18.3%; Score 95.4; DB 10; Length 255;

Best Local Similarity 78.5%; Pred. No. 2.3e-21;

Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;

QY 82 TTATAGTCTGTAGCTCAGTGGTTAGAGCGCACCCCTGATAAGGTTGAGGTGCGGAGTT 141

Db 159 TAATGGCCCTATAGCTCAGCTGAGTTAGAGCGCACCCCTGATAAGCGTGAGTGGTGGTT 100

QY 142 CAAATCTGCCAGACCTACCAATTGCTTGTGAGAGAGATACGGGGCCATAGCTCAGCT 201

Db 99 CGAGTCCACTTAGGCCCCACCATTAAATTT----AATACCTATTGGGGGCTTAGCTCAGCT 44

QY 202 GGGAGAGCGCGCTGCTTGCACGAGAGGTCAGCGGTTTCGATC 244

Db 43 GGGAGAGCGCGCTGCTTGCACGAGAGGTCAGCGGTTTCGATC 1

## RESULT 15

US-09-815-242-1638/c

; Sequence 1638, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1638

; LENGTH: 255

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-09-815-242-1638

Query Match 18.3%; Score 95.4; DB 10; Length 255;

Best Local Similarity 78.5%; Pred. No. 2.3e-21;

Matches 128; Conservative 0; Mismatches 31; Indels 4; Gaps 1;

QY 82 TTATAGTCTGTAGCTCAGTGGTTAGAGCGCACCCCTGATAAGGTTGAGGTGCGGAGTT 141

Db 159 TAATGGCCCTATAGCTCAGCTGAGTTAGAGCGCACCCCTGATAAGCGTGAGTGGTGGTT 100

QY 142 CAAATCTGCCAGACCTACCAATTGCTTGTGAGAGAGATACGGGGCCATAGCTCAGCT 201

Db 99 CGAGTCCACTTAGGCCCCACCATTAAATTT----AATACCTATTGGGGGCTTAGCTCAGCT 44

QY 202 GGGAGAGCGCGCTGCTTGCACGAGAGGTCAGCGGTTTCGATC 244

Db 43 GGGAGAGCGCGCTGCTTGCACGAGAGGTCAGCGGTTTCGATC 1

Search completed: February 1, 2003, 06:51:14

Job time : 248.936 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:09:56 ; Search time 970.301 Seconds  
(without alignments)  
8679.427 Million cell updates/sec

Title: US-09-931-486-112

Perfect score: 520

Sequence: 1 ATCGAGACATCAGCTTCTT.....CAGATTGCTGGGGTTATAT 520

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	178.6	34.3	507	17	BH200120
C 2	175.4	33.7	629	17	BH201541
C 3	170.8	32.8	639	17	AQ509640
C 4	124.4	23.9	319	10	BE092111
C 5	77	14.8	754	17	BH405252
C 6	73	14.0	593	17	BH400944

C 7	73	14.0	760	17	BH393190
C 8	69.4	13.3	619	9	AA680996
C 9	69.4	13.3	6499	17	BH771024
C 10	67.8	13.0	497	13	BI544108
C 11	67.8	13.0	548	13	BI544155
C 12	66.8	12.8	577	17	BH819575
C 13	66.2	12.7	539	13	BI544086
C 14	63.8	12.3	287	17	BH614410
C 15	62.6	12.0	191	17	AZ578476
C 16	62.6	12.0	712	17	BH397037
C 17	58.6	11.3	579	17	BH375975
C 18	57.2	11.0	608	17	BH375641
C 19	54.6	10.5	696	17	BH383241
C 20	53.6	10.3	679	13	BI263958
C 21	52.6	10.1	541	17	BH387664
C 22	52.6	10.1	774	12	BG354849
C 23	52.4	10.1	617	9	AI526132
C 24	51.8	10.0	713	13	BH096963
C 25	50.6	9.7	2149	17	AQ012191
C 26	49.6	9.5	551	10	BE092053
C 27	49.4	9.5	612	17	AQ989869
C 28	49.2	9.5	653	13	BH318992
C 29	48.2	9.3	501	13	BH313245
C 30	48	9.2	372	10	BE092243
C 31	47.6	9.2	1258	17	BH770957
C 32	47.6	9.2	3268	17	BH770998
C 33	46.6	9.0	938	17	AZ683938
C 34	46.4	8.9	461	17	BH644007
C 35	45.8	8.8	874	17	CNS066SM
C 36	45.6	8.8	904	17	BH159957
C 37	45.4	8.7	715	17	BH375497
C 38	45.2	8.7	907	17	CNS06M2C
C 39	45	8.7	876	17	CNS06T5R
C 40	45	8.7	902	17	CNS06M5P
C 41	45	8.7	1047	17	CNS06XDL
C 42	44.8	8.6	197	17	BH855109
C 43	44.8	8.6	216	17	BH169234
C 44	44.8	8.6	330	14	BQ205940
C 45	44.4	8.5	432	13	BI941477

#### ALIGNMENTS

RESULT 1  
BH200120/c  
LOCUS  
Sml-57J2.TF Sml Schistosoma mansoni genomic clone Sml-57J2, DNA  
DEFINITION  
sequence.  
ACCESSION  
BH200120  
VERSION  
BH200120.1 GI:16370164  
KEYWORDS  
GSS.  
SOURCE  
Schistosoma mansoni.  
ORGANISM  
Schistosoma mansoni  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.  
REFERENCE  
1 (bases 1 to 507)  
AUTHORS  
Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed ,N.M.  
TITLE  
Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sml BAC library for gene discovery and map construction  
JOURNAL  
Unpublished (2001)  
COMMENT  
Other\_GSSs: Sml-57J2.TR  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
lo.edu).  
Seq primer: M13 For  
Class: BAC ends.





into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

73 a 62 c 91 g 93 t

BASE COUNT  
ORIGIN

Query Match 23.9%; Score 124.4; DB 10; Length 319;  
Best Local Similarity 68.0%; Pred. No. 1.2e-27;  
Matches 208; Conservative 0; Mismatches 86; Indels 12; Gaps 2;

QY 99 AGTTGGTTAGAGCCGCCCTGATAAGGTCAGGTGCGCAGTTCAAATCTGCCAGACCT 158  
|||||  
Db 1 AGTTGGTTAGAGCCGCCCTTTGATAAGGTCAGGTGCGCAGTTCGAATCTGCCAGACCC 60  
|||||

QY 159 ACCAATTCCTGGTCGAGAAG-----AATACGGGGCCATAGCTCAGCTGGGAGAGCG 210  
|||||  
Db 61 ACCAATTCCTGGCGGAAAGCCCTGTAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCG 120  
|||||

QY 211 CTGTCCTTGCACGAGAGGTACGGGTTCGATCCCGGTTGGCTCCACCACTCTCTCGTG 270  
|||||  
Db 121 CTTGCCCTTGCACGAGAGGTCAACGGTTTCGATCCCGGTTGGCTCCACCACTTACGTTGT 180  
|||||

QY 271 TTGGCGGTGAGTGTAAAG---AGTTCAGAAATGATGCCGCTTCAGGTTTGCCTGTGA 326  
|||||  
Db 181 GATGGTGTGGCTGTAGTTCCTCTCGGTTAGAGTTTGAATAAGCATTCATCGC 240  
|||||

QY 327 GTGCTGATTTCTGGCTTTTACCGGTACGAAATCTCTTTAAAAATTTGGATATGTG 386  
|||||  
Db 241 GATGGTGAATGTGATTTCTAGTCTTTGATTAGATCGTTCTTTACAAATTTGGGTATGTG 300  
|||||

QY 387 ATAGAA 392  
|||||  
Db 301 ATAGAA 306

RESULT 5  
BH405252/c

LOCUS AG-ND-127K13.TR ND-TAM Anopheles gambiae genomic clone AG-ND-127K13  
DEFINITION AG-ND-127K13.TR ND-TAM Anopheles gambiae genomic clone AG-ND-127K13  
DNA sequence.

ACCESSION BH405252

VERSION BH405252.1 GI:17351468

KEYWORDS GSS.

SOURCE African malaria mosquito.

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Anopheles.

REFERENCE 1 (bases 1 to 754)

AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.

TITLE Direct Submission of BAC-end sequences from Anopheles gambiae

JOURNAL Unpublished (2001)

COMMENT Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: b.loftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by

F.H. Collins and sequenced by The Institute for Genomic Research

(TIGR). The BAC library was generated from A. gambiae PEST strain

DNA. All DNA was extracted from newly hatched first instar larvae

to minimize the inclusion of DNA from microorganisms that inhabit

the gut. The DNA is derived from mixed sexes of larvae. The BAC

library was constructed at Texas A&M University BAC Center

University, College Station, Texas 77843-2123, USA using a HindIII

partial digest.

Seq primer: M13 Rev

Class: BAC ends.

FEATURES  
source

Location/Qualifiers

1..754

/organism="Anopheles gambiae"

/strain="PEST"

/db\_xref="taxon:7165"

/clone="AG-ND-127K13"

/clone\_lib="ND-TAM"

/note="Vector: pECBAC1; Site\_1: HindIII"

BASE COUNT 180 a 199 c 167 g 208 t

ORIGIN

Query Match 14.8%; Score 77; DB 17; Length 754;

Best Local Similarity 64.9%; Pred. No. 1.2e-12;

Matches 150; Conservative 0; Mismatches 70; Indels 11; Gaps 2;

RESULT 6  
BH400944/c

LOCUS AG-ND-158022.TF ND-TAM Anopheles gambiae genomic clone AG-ND-158022

DEFINITION AG-ND-158022.TF ND-TAM Anopheles gambiae genomic clone AG-ND-158022

DNA sequence.

ACCESSION BH400944

VERSION BH400944.1 GI:17347147

KEYWORDS GSS.

SOURCE African malaria mosquito.

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Anopheles.

REFERENCE 1 (bases 1 to 593)

AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.

TITLE Direct Submission of BAC-end sequences from Anopheles gambiae

JOURNAL Unpublished (2001)

COMMENT Other\_GSSs: AG-ND-158022.TR

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: b.loftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by

F.H. Collins and sequenced by The Institute for Genomic Research

(TIGR). The BAC library was generated from A. gambiae PEST strain

DNA. All DNA was extracted from newly hatched first instar larvae

to minimize the inclusion of DNA from microorganisms that inhabit

the gut. The DNA is derived from mixed sexes of larvae. The BAC

library was constructed at Texas A&M University BAC Center

University, College Station, Texas 77843-2123, USA using a HindIII

partial digest.

Seq primer: M13 For

Class: BAC ends.

FEATURES  
source

Location/Qualifiers

1..593

/organism="Anopheles gambiae"

/strain="PEST"

/db\_xref="taxon:7165"

/clone="AG-ND-158022"

/clone\_lib="ND-TAM"

/note="Vector: pECBAC1; Site\_1: HindIII"

```

BASE COUNT      119 a      157 c      118 g      199 t
ORIGIN
Query Match      14.0%; Score 73; DB 17; Length 593;
Best Local Similarity 69.4%; Pred. No. 1.8e-11;
Matches 134; Conservative 0; Mismatches 45; Indels 14; Gaps 2;

QY  92 GTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTCGGCAGTTCAAAATCTGCC 151
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db  574 GTAGCTCAGTTGGTTAGAGCGCTACACTGATAATAGAGGTGCGGCGAGTTTCGAGCTGCC 515
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY  152 CAGACTACCAATGCTTGGTCGAGAAGAAATACGGGGCCATAGCTCAGCTGGG-GAGAGCG 210
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db  509 CGAGACTACTAAT-----GAAAAGGGGAATTAGCTCAGCTGGGTAGAGCG 463
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY  211 CCTGCTTCACGACGAGGAGGTTCGATCCCGCTGGCTCCACCACTCTCTCGTG 270
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db  462 CCTGCTTCACGACGAGGTCAGAGGTTTCGACTCCCTTATCTCCACAGTTTGTGGA 403
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY  271 TTGCGGTGAGTGT 283
||  |||  |
Db  402 CTGATACAAGTAT 390
||  |||  |

RESULT 8
AA680996/c
LOCUS
DEFINITION
  619 bp      mRNA      linear      EST 30-DEC-1997
  (SAW97MLW-Bml3d9) Brugia malayi cDNA clone SW3D9CA514 5', mRNA
  sequence.
ACCESSION      AA680996
VERSION        AA680996.1 GI:2663001
KEYWORDS
SOURCE
  Brugia malayi.
  Brugia malayi.
ORGANISM
  Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
  Onchocercidae; Brugia.
  1 (bases 1 to 619)
REFERENCE
  Williams, S.A. and Lizotte-Waniewski, M.
  Genes expressed in day 9 post-infection, third stage larvae of
  Brugia malayi
  Unpublished (1997)
JOURNAL
COMMENT
  Molecular Parasitology
  Smith College Department of Biological Sciences
  Department of Biological Sciences, Clark Science Center, Smith
  College, Northampton, MA, 01063, USA
  Tel: 4135853826
  Fax: 4135853786
  Email: genome@smith.edu
  Seq primer: pBluescript SK.
  Location/Qualifiers
    1..619
      /organism="Brugia malayi"
      /db_xref="taxon:6279"
      /clone="SW3D9CA514"
      /clone_lib="Brugia malayi L3 molting-day 9 larva cDNA
      (SAW97MLW-Bml3d9)"
      /dev_stage="third stage larvae, nine days after infection"
      /lab_host="E. coli XL1-Blue MRF"
      /note="Vector: LambdaZap II (Unizap XR); Site_1: Eco RI
      (5' end); Site_2: Xho I (3' end); Brugia malayi is a
      lymphatic filarial nematode parasite of humans. mRNA was
      prepared from third stage larvae of Brugia malayi
      isolated from the peritoneal cavity of jirds nine days
      after infection. The mRNA was converted to double
      stranded cDNA using reverse transcriptase and oligo (dT)
      followed by Rnase H and DNAPol I. The library was
      constructed by Michelle Lizotte-Waniewski. The library is
      available from the Filarial Genome Project Resource Center,
      Center: contact Dr. S.A. Williams, Clark Science Center,
      Smith College, Northampton, MA 01063 USA phone +1 413
      585-3826 fax +1 413 585-3786 email genome@smith.edu"

BASE COUNT      148 a      148 c      121 g      168 t
ORIGIN
Query Match      13.3%; Score 69.4; DB 9; Length 619;
Best Local Similarity 69.9%; Pred. No. 2.5e-10;

BASE COUNT      119 a      157 c      118 g      199 t
ORIGIN
Query Match      14.0%; Score 73; DB 17; Length 760;
Best Local Similarity 69.4%; Pred. No. 2.2e-11;
Matches 134; Conservative 0; Mismatches 45; Indels 14; Gaps 2;

QY  92 GTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTCGGCAGTTCAAAATCTGCC 151
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db  574 GTAGCTCAGTTGGTTAGAGCGCTACACTGATAATAGAGGTGCGGCGAGTTTCGAGCTGCC 515
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY  152 CAGACTACCAATGCTTGGTCGAGAAGAAATACGGGGCCATAGCTCAGCTGGG-GAGAGCG 210
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db  514 CGAGACTACTAAT-----GAAAAGGGGAATTAGCTCAGCTGGGTAGAGCG 468
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY  211 CCTGCTTCACGACGAGGAGGTTCGATCCCGCTGGCTCCACCACTCTCTCGTG 270
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db  467 CTGCTTCACGACGAGGTCAGAGGTTTCGACTCCCTTATCTCCACAGTTTGTGGA 408
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY  271 TTGCGGTGAGTGT 283
||  |||  |
Db  407 CTGATACAAGTAT 395
||  |||  |

RESULT 7
BH393190/c
LOCUS
DEFINITION
  760 bp      DNA      linear      GSS 11-DEC-2001
  AG-ND-168H12.TR ND-TAM Anopheles gambiae genomic clone AG-ND-168H12
  , DNA sequence.
ACCESSION      BH393190
VERSION        BH393190.1 GI:17339331
KEYWORDS
  GSS.
SOURCE
  African malaria mosquito.
  Anopheles gambiae
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
  Anopheles.
  1 (bases 1 to 760)
REFERENCE
  Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.
  Direct Submission of BAC-end sequences from Anopheles gambiae
  Unpublished (2001)
JOURNAL
COMMENT
  Other_GSSs: AG-ND-168H12.TF
  Department of Eukaryotic Genomics
  Contact: Brendan J Loftus
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0208
  Fax: 301 838 3543
  Email: bjloftus@tigr.org
  This clone is from an A. gambiae BAC library (ND-TAM) provided by
  F.H. Collins and sequenced by The Institute for Genomic Research
  (TIGR). The BAC library was generated from A. gambiae PEST strain
  DNA. All DNA was extracted from newly hatched first instar larvae
  to minimize the inclusion of DNA from microorganisms that inhabit
  the gut. The DNA is derived from mixed sexes of larvae. The BAC
  library was constructed at Texas A&M University BAC Center
  University, College Station, Texas 77843-2123, USA using a HindIII
  partial digest.
  Seq primer: M13 Rev
  Class: BAC ends.
  Location/Qualifiers
    1..760
      /organism="Anopheles gambiae"
      /strain="PEST"
      /db_xref="taxon:7165"
      /clone="AG-ND-168H12"
      /clone_lib="ND-TAM"
      /note="Vector: pECBAC1; Site_1: HindIII"

BASE COUNT      171 a      187 c      139 g      263 t
ORIGIN
Query Match      14.0%; Score 73; DB 17; Length 760;
Best Local Similarity 69.4%; Pred. No. 2.2e-11;

```

Matches 130; Conservative 0; Mismatches 34; Indels 22; Gaps 2;

QY 97 TCAGTGTAGAGCGCACCCCTGATAGAGGTGAGGTGGCGAGTTCAAATCTGCCAGAC 156  
 Db 518 TCAGTGTAGAGCGCACCCCTGATAGAGGTGAGGTGGGTTCAGTCCACTCAGGC 459  
 QY 157 CTACCAATT-----GCTTGTGCGAGAAGATACGGGCCCATAGCT 196  
 Db 458 CTACCAATTTGCACGGCAAAATTTGAAGAGGTTTAACTACATGCTATGGGTTATAGCT 399  
 QY 197 CAGCTGGGAGAGCGCTCCCTTGA--CGCAGGAGTACGGTTCGATCCCGCTGGCT 254  
 Db 398 CAGCTGGGAGAGCGCTCCCTTGGATCGCAGGAGTCCCGTTGATCCCGCTNGCT 339  
 QY 255 CCACCA 260  
 Db 338 CCACCA 333

RESULT 9  
 BH771024  
 LOCUS  
 DEFINITION LMGtag746 MGI363 Random Sequence Tag Library Lactococcus lactis  
 subsp. cremoris genomic, DNA sequence.

ACCESSION BH771024  
 VERSION BH771024.1 GI:20373981  
 KEYWORDS GSS.

SOURCE Lactococcus lactis subsp. cremoris.  
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 Lactococcus.

REFERENCE 1 (bases 1 to 6499)  
 Bolotin,A., Glitch,S.D. and Sorokin,A.  
 TITLE Studies of genomes of dairy bacteria Lactococcus lactis  
 JOURNAL Sci. Aliment., (2002) In press  
 COMMENT Contact: Sorokin A  
 Genetique Microbienne  
 INRA

CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France  
 Tel: 33 1 34 65 25 16  
 Fax: 33 1 34 65 25 21  
 Email: sorokine@jouy.inra.fr  
 best homologue in strain IL1403 is ywga (78%)  
 Class: shotgun  
 High quality sequence start: 30  
 High quality sequence stop: 6471.

FEATURES  
 source  
 1..6499  
 Location/Qualifiers

/organism="Lactococcus lactis subsp. cremoris"  
 /strain="MGI363"  
 /db\_xref="taxon:1359"  
 /clone\_lib="MGI363 Random Sequence Tag Library"  
 /notes="Vector: pSGM02; Site\_1: SmaI; Library of  
 chromosomal fragments of L.lactis strain MGI363 was  
 prepared by partial AluI digestion or by sonication."  
 BASE COUNT 1946 a 1228 c 1683 g 1642 t

Query Match 13.3%; Score 69.4; DB 17; Length 6499;  
 Best Local Similarity 92.4%; Pred. No. 1.2e-09;  
 Matches 73; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 179 GAATCGGGGCCATAGCTACGTGGGAGAGCGCTGCTGACGACGAGGAGTACGGGT 238  
 Db 2159 GATGTGGGGCCCTAGCTAGCTGGGAGAGCGCTGCTGTTGACGACGAGGAGTACGGGT 2218

QY 239 TCATCCCGCTTGGCTCCA 257  
 Db 2219 TCATCCCGCTAGGCTCCA 2237

RESULT 10  
 BI544108

LOCUS  
 DEFINITION BI544108 497 bp mRNA linear EST 01-MAR-2002  
 lemameiformis cdna 5', mRNA sequence.

ACCESSION BI544108  
 VERSION BI544108.1 GI:19033790  
 KEYWORDS EST.  
 SOURCE Gracilaria lemameiformis.

ORGANISM Gracilaria lemameiformis.  
 Eukaryota; Rhodophyta; Florideophyceae; Gracilariaceae; Gracilariaceae; Gracilaria.

REFERENCE 1 (bases 1 to 497)  
 Sun,X., Yang,G.P., Mao,Y.X. and Zhang,X.C.  
 TITLE Analysis of expressed sequence tags of a marine red alga,  
 Gracilaria lemameiformis

JOURNAL Unpublished (2001)  
 COMMENT Contact: Sun, X.; Zhang, X. C.  
 College of Marine Life Sciences

Ocean University of Qingdao  
 Yushan Road 5, Qingdao, 266003, Shandong, China  
 Tel: +86-0532-2032789

Fax: +86-0532-2032276  
 Email: xczhang@ouqd.edu.cn

PCR Primers  
 FORWARD: 5' -CGTGTACCATGCTCTAGAGT-3'

BACKWARD: 5' -CTGATCTAGACCTCAGGCTC-3'

Seq primer: 5' -CGTGTACCATGCTCTAGAGT-3'

POLYA-No.

Location/Qualifiers

1..497

/organism="Gracilaria lemameiformis"

/db\_xref="taxon:2778"

/clone\_lib="Gracilaria lemameiformis gametophyte cdna  
 library"

/tissue\_type="gametophyte thalli"

/note="Vector: pMD 18-T; Site\_1: EcoR V with a T hang;  
 Wild type Gracilaria lemameiformis were harvested from  
 Zhanshan Bay, Qingdao (China). After rinsed with boiled  
 seawater, younger thalli was cut and washed every 3-4  
 days until 1 month. Then thalli was cultivated in  
 Provasoli medium. Total RNA was isolated from thalli of  
 gametophyte algae, using UNIQ-10 Trizol total RNA  
 Preparation Kit(Sangon Inc., Shanghai, China). The cdna  
 was synthesized, amplified and cloned using cdna  
 Synthesis Kit, cdna PCR Library Kit and pMD 18-T vector  
 (Takara Biotechnology Co., Ltd., Dalian, China),  
 respectively."

BASE COUNT 151 a 77 c 103 g 166 t

ORIGIN

Query Match 13.0%; Score 67.8; DB 13; Length 497;  
 Best Local Similarity 69.1%; Pred. No. 6.8e-10;  
 Matches 114; Conservative 0; Mismatches 37; Indels 14; Gaps 1;

QY 93 TAGCTCAGTTGGTTAGAGCGCACCCCTGTAGAGGTGAGTGGCAGTTCAAATCTGCC 152  
 Db 232 TAGCTCAGTTGGTTAGAGCGCACCCCTGTAGAGGTGAGTGGTTCAAATCCAGGA 291

QY 153 AGACCTACCAATTGCTTGGTCGAGAAGATACGGGGCGATAGCTCAGCTGGGAGAGCGCC 212  
 Db 292 TAGCCACCATGA-----ATAAGGGGGTATAGCTCAGCTGGTAGAGCGCT 337

QY 213 TGCCTTGACCGAGGAGGTGAGCGGTTCGATCCCGTTGGCTCCA 257  
 Db 338 GCTTTTGAAGCAGATGTCAGCGGTTCAAATCCGCTTATCTCCA 382

RESULT 11  
 BI544155

LOCUS

DEFINITION BI544155 548 bp mRNA linear EST 01-MAR-2002  
 S129 Gracilaria lemameiformis gametophyte cdna library Gracilaria  
 lemameiformis cdna 5', mRNA sequence.

ACCESSION BI544155

VERSION BI544155.1 GI:19033837





/note="Vector: pMD 18-T; Site\_1: EcoR V with a T hang; Wild type Gracilaria lemaneiformis were harvested from Zhanshan Bay, Qingdao (China). After rinsed with boiled seawater, younger thalli was cut and washed every 3-4 days until 1 month. Then thalli was cultivated in Provasoli medium. Total RNA was isolated from thalli of gametophyte algae, using UNIQ-10 Trizol Total RNA Preparation Kit (Sangon Inc., Shanghai, China). The cDNA was synthesized, amplified and cloned using cDNA Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector (Takara Biotechnology Co., Ltd., Dalian, China), respectively."

BASE COUNT 179 a 89 c 109 g 162 t  
ORIGIN

Query Match 12.7%; Score 66.2; DB 13; Length 539;  
Best Local Similarity 68.5%; Pred. No. 2.3e-09;  
Matches 113; Conservative 0; Mismatches 38; Indels 14; Gaps 1;

QY 93 TAGCTCAGTTGTTAGAGCGCACCCCTGATAGGGTGAGTGGCGAGTTCAAATCTGCC 152  
DB 73 TAGCTCAGTTGTTAGAGCGCACCCCTGATAGGGTGAGTGGCGAGTTCAAATCTGCC 132

QY 153 AGACCTACCAATGCTGTGTCGAGAGATACGGGCCCATAGCTCAGCTGGGAGAGCGCC 212  
DB 133 TAGCCCCACATGA-----ATAAGGGGGGTATAGCTCAGCTGGTGTAGAGTGCT 178

QY 213 TGCCTTGCAGCAGGAGGTGAGCGGTTCGATCCCGCTTGGCTCCA 257  
DB 179 GCTTTTGAAGCAGATGTCAGCGGTTCAAATCCCGTTATCTCCA 223

RESULT 14  
BH614410  
LOCUS 287 bp DNA linear GSS 07-JAN-2002  
DEFINITION 1C22AG2 Subclones from overlapping BAC clones spanning the hrp cluster of Erwinia carotovora subsp. atroseptica Pectobacterium carotovorum subsp. atrosepticum genomic, DNA sequence.

ACCESSION BH614410  
VERSION BH614410.1 GI:18078210  
KEYWORDS GSS.  
SOURCE Pectobacterium carotovorum subsp. atrosepticum.  
ORGANISM Pectobacterium carotovorum subsp. atrosepticum.  
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae; Pectobacterium.

REFERENCE 1 (bases 1 to 287)  
AUTHORS Bell, K.S., Avrova, A.O., Holvea, M.C., Cardle, L., Morris, W., De Jong, W., Toth, I.K., Waugh, R., Bryan, G.J., and Birch, P.R.J.  
TITLE Sample sequencing of a selected region of the genome of Erwinia carotovora subsp. atroseptica reveal candidate phytopathogenicity genes and allows comparison with Escherichia coli Unpublished (2002)

JOURNAL Contact: Bell KS  
COMMENT Scottish Crop Research Institute  
Invergowrie, Dundee, United Kingdom, DD2 5DA  
Email: kbells@scri.sari.ac.uk  
Class: BAC subclone.

FEATURES location/Qualifiers  
1..287  
/organism="Pectobacterium carotovorum subsp. atrosepticum"  
/strain="SCRI1039"  
/db\_xref="taxon:29471"  
/clone\_lib="Subclones from overlapping BAC clones spanning the hrp cluster of Erwinia carotovora subsp. atroseptica"  
/note="Vector: pGEM 3zf; DNA from BAC clones Eca2B8 and EcalC22 was nebulised and cloned into pGEM 3zf and sequenced with SP6 or T7 primers"  
74 a 62 c 78 g 73 t

BASE COUNT 74 a 62 c 78 g 73 t  
ORIGIN

Query Match 12.3%; Score 63.8; DB 17; Length 287;  
Best Local Similarity 85.5%; Pred. NO. 8.4e-09;  
Matches 71; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 83 TATAGGCTGTAGCTCAGTTGTTAGAGCGCACCCCTGATAAGGGTGAGGTGCGCAGTTC 142  
DB 170 TACAGGCTGTAGCTCAGTTGTTAGAGCGCACCCCTGATAAGGGTGAGGTGCGTGGTTC 229

QY 143 AAATCTGCCAGACCTACCAATT 165  
DB 230 AAGTCCACTCAGCGCTACCAAT 252

RESULT 15  
AZ578476/c  
LOCUS 191 bp DNA linear GSS 08-DEC-2000  
DEFINITION 23h03 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium sp. NGR234 genomic clone 23h03, DNA sequence.

ACCESSION AZ578476  
VERSION AZ578476.1 GI:11605796  
KEYWORDS GSS.  
SOURCE Rhizobium sp. NGR234.  
ORGANISM Rhizobium sp. NGR234.

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium.

REFERENCE 1 (bases 1 to 191)  
AUTHORS Viprey, V., Rosenthal, A., Broughton, W.J. and Perret, X.  
TITLE Genetic snapshots of the Rhizobium species NGR234 genome  
JOURNAL Genome Biol. 1 (6), RESEARCH0014 (2000)  
MEDLINE 21114532  
COMMENT Contact: Virginie Viprey  
Laboratoire de Biologie Moleculaire des Plantes Superieures  
University of Geneva

1 Chemin de l'Imperatrice, Chambesy/Geneva 1292, Switzerland  
Tel: +44 (0)1603450000  
Fax: +44 (0)1603450045  
Email: virginie.viprey@bbrc.ac.uk  
Class: shotgun.  
Location/Qualifiers  
1..191  
/organism="Rhizobium sp. NGR234"  
/strain="ANU265"  
/db\_xref="taxon:394"  
/clone="23h03"  
/clone\_lib="Shot-gun genomic library of Rhizobium strain ANU265"  
/note="Vector: M13; derivative strain of NGR234 cured of pNGR234a"

BASE COUNT 47 a 62 c 44 g 37 t 1 others  
ORIGIN

Query Match 12.0%; Score 62.6; DB 17; Length 191;  
Best Local Similarity 87.2%; Pred. No. 1.5e-08;  
Matches 68; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 185 GGGCCCATAGCTCAGCTGGGAGAGCGCTTGCAGCGCAGGAGGTTCAGCGTTCGATC 244  
DB 111 GGGCTGTAGCTCAGCTGGGAGAGCACATGCTTTCAGACAGGGGGTTCAGCGTTCGATC 52

QY 245 CCGCTTGGCTCCCACT 262  
DB 51 CCGCTCAGCTCCCACT 34

Search completed: February 1, 2003, 04:21:54  
Job time : 976.301 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:06:21 : Search time 1037.68 Seconds  
(without alignments)  
14135.156 Million cell updates/sec

Title: US-09-931-486-113

Perfect score: 504

Sequence: 1 ATCGAAGACACCGGCTTCGT.....CAGATTGCTGGGGTTATAT 504

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rtd.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	504	100.0	504	6	A48046	A48046 Sequence 11
2	504	100.0	504	6	AX177091	AX177091 Sequence
3	504	100.0	504	6	AX191054	AX191054 Sequence
4	504	100.0	505	1	PST251910	PST251910 Pseudomon
5	502.4	99.7	505	1	PST390584	AJ390584 Pseudomon
6	500.4	99.3	505	1	PST390585	AJ390585 Pseudomon
7	500	99.2	505	1	PST390582	AJ390582 Pseudomon
8	499.2	99.0	505	1	PST390583	AJ390583 Pseudomon
9	489.6	97.1	505	1	PST251900	AJ251900 Pseudomon
10	486.6	96.5	506	1	PST251908	AJ251908 Pseudomon
11	483.4	95.9	506	1	PST390588	AJ390588 Pseudomon
12	345.4	68.5	528	1	PST251905	AJ251905 Pseudomon
13	344.2	68.3	528	1	PST251903	AJ251903 Pseudomon
14	342.6	68.0	528	1	PST390589	AJ390589 Pseudomon
15	341.6	67.8	529	1	PST251904	AJ251904 Pseudomon
16	341.6	67.8	529	1	PST390587	AJ390587 Pseudomon
17	307.6	61.0	530	1	PST251907	AJ251907 Pseudomon
18	306	60.7	530	1	PST251906	AJ251906 Pseudomon
19	305.2	60.6	560	1	AF356514	AF356514 Pseudomon
20	287	56.9	529	1	PST251901	AJ251901 Pseudomon
21	287	56.9	529	1	PST251902	AJ251902 Pseudomon
22	284.2	56.4	529	1	PST390590	AJ390590 Pseudomon
23	268.6	53.3	5785	1	PSU65012	U65012 Pseudomonas
24	265.4	52.7	499	6	A48047	A48047 Sequence 11
25	265.4	52.7	499	6	AR177092	AR177092 Sequence
26	265.4	52.7	499	6	AX191055	AX191055 Sequence
27	264	52.4	523	1	PST390581	AJ390581 Pseudomon
28	249	49.4	520	6	A48045	A48045 Sequence 11
29	249	49.4	520	6	AR177090	AR177090 Sequence
30	249	49.4	520	6	AX191053	AX191053 Sequence
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32	225.8	44.8	471	6	A48044	A48044 Sequence 11
33	225.8	44.8	471	6	AR177089	AR177089 Sequence
34	225.8	44.8	471	6	AX191052	AX191052 Sequence
35	222.4	44.1	707	1	PSEDFO	L28162 Pseudomonas
36	221	43.8	528	1	PAE439391	AJ439391 Pseudomon
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C 38	221	43.8	12065	1	AE004883	AE004883 Pseudomon
39	217.6	43.2	705	1	PSEDFM	L28160 Pseudomonas
40	214.4	42.5	705	1	PSEDFN	L28161 Pseudomonas
41	213.2	42.3	498	1	PAE439392	AJ439392 Pseudomon
42	212.2	42.1	521	1	PAE439389	AJ439389 Pseudomon
43	212.2	42.1	544	1	AF083211	AF083211 Azotobact
44	210.8	41.8	533	1	AF079808	AF079808 Azotobact
45	209	41.5	531	1	PAE439388	AJ439388 Pseudomon

#### ALIGNMENTS

RESULT 1  
A48046  
LOCUS A48046  
DEFINITION Sequence 113 from Patent WO9600298.  
ACCESSION A48046  
VERSION A48046.1 GI:2301908  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 504)  
AUTHORS James G., Rossau, R. and Van H.H.  
TITLE SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF  
EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY  
JOURNAL Patent: WO 9600298-A 113 04-JAN-1996;

504 bp DNA linear PAT 07-MAR-1997

INNOGENETICS NV (BE)  
Other publication AU 2924695 960119.

FEATURES  
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BASE COUNT 119 a 111 c 137 g 137 t

Query Match 100.0%; Score 504; DB 6; Length 504;

Best Local Similarity 100.0%; Pred. No. 5.1e-140;

Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACACCGGCTTCGTCATAGCTCCACACGAAATTCGTCGATTCACCTTGGGAAAG 60

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QY 361 TGGTATGTGATGAAGTAGACCGATGTTGCTTTCACTGGCAGCATGTCGCGTCAAGG 420

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QY 421 TAAATTTGGCTGTTCTATGCAAAATTTTCGGGGAATGTCGTTTCACTGGCAGCATGTCGCGTCAAGG 480

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QY 481 TAACAGATTGCTTGGGTTATAT 504

Db 481 TAACAGATTGCTTGGGTTATAT 504

#### RESULT 2

AR177091 LOCUS 504 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 113 from patent US 6312903.

ACCESSION AR177091

VERSION AR177091.1 GI:17919446

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 504)

AUTHORS James G., Rossau, R. and Van Heuverswyn, H.

TITLE Simultaneous detection, identification and differentiation of

subcellular taxa using a hybridization assay

JOURNAL Patent: US 6312903-A 113 06-NOV-2001;

FEATURES

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/db\_xref="taxon:32644"

BASE COUNT 119 a 111 c 137 g 137 t

ORIGIN

Query Match 100.0%; Score 504; DB 6; Length 504;

Best Local Similarity 100.0%; Pred. No. 5.1e-140;

Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 TAACAGATTGCTTGGGTTATAT 504

Db 481 TAACAGATTGCTTGGGTTATAT 504

#### RESULT 3

AX191054 LOCUS 504 bp DNA linear PAT 10-AUG-2001

DEFINITION Sequence 113 from Patent EP1091004.

ACCESSION AX191054

VERSION AX191054.1 GI:15149699

KEYWORDS

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 504)

AUTHORS James G., Rossau, R. and van Heuverswyn, H.

TITLE Simultaneous detection, identification and differentiation of

subcellular taxa using a hybridization assay

JOURNAL Patent: EP 1091004-A 113 11-APR-2001;

FEATURES

source 1..504

/db\_xref="taxon:32644"

BASE COUNT 119 a 111 c 137 g 137 t

ORIGIN

Query Match 100.0%; Score 504; DB 6; Length 504;

Best Local Similarity 100.0%; Pred. No. 5.1e-140;

Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATCGAAGACACCGGCTTCGTCATAGCTCCACACGAAATTCGTCGATTCACCTTGGGAAAG 60

QY 61 GCGATTGGGTTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120

Db 61 GCGATTGGGTTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120

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QY 121 CCCCTGATAAGGTTGAGTGGCGAGTTCTGAATCTGCCAGACCCACCAATCGAAGGGGCC 180
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Db 361 TGGGTATGTATAGAACTAGACCGATGTTGCTTTACCTGCGAGCATGTCGCGTCAAGG 420
QY 421 TAAATTTGCGTCTCTCTATGCAATTTTCGGCGAATGTCGCTTCACGTTATAGACAG 480
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QY 481 TAACCAAGATGCTGGGGTTATAT 504
Db 481 TAACCAAGATGCTGGGGTTATAT 504

RESULT 4
PST251910
LOCUS
DEFINITION
Pseudomonas stutzeri internal transcribed spacer 1 (ITS1),trna-Ile
and trna-Ala, strain CCUG 11256-T.
ACCESSION
AJ251910
VERSION
AJ251910.1 GI:9844598
KEYWORDS
RNA-Ile; trna-Ala; trna-Ile.
SOURCE
Pseudomonas stutzeri.
ORGANISM
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE
1 (bases 1 to 505)
Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.
Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
20393664
PUBMED
10939670
REFERENCE
2 (bases 1 to 505)
Bannasar,A.
Direct Submission
Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
Location/Qualifiers
1. .505
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/strain="CCUG 11256-T"
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93. .169
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QY 61 GCGATTGGGTTTACACCGGAGTAACGATTGGGTCTCTAGCTCAGTTGGTTAGAGCCGA 120
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Db 482 TAACCAAGATGCTGGGGTTATAT 505

PST390584
Pseudomonas stutzeri intergenic spacer, trna-Ile and trna-Ala
genes, strain SD93936.
ACCESSION
AJ390584
VERSION
AJ390584.1 GI:9844624
KEYWORDS
IGS; intergenic spacer; transfer RNA Ile; transfer RNA-Ala;
trna-Ala gene; trna-Ile gene.
SOURCE
Pseudomonas stutzeri.
ORGANISM
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE
1 (bases 1 to 505)
Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.
Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
20393664
PUBMED
10939670
REFERENCE
2 (bases 1 to 505)
Bannasar,A.
Direct Submission
Submitted (15-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
Location/Qualifiers
1. .505
JOURNAL
MEDLINE
PUBMED
10939670
AUTHORS
Bannasar,A.
TITLE
Direct Submission
JOURNAL
Submitted (15-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
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177. .251  
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/anticodon=(pos:204. .206,aa:ala)  
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Best Local Similarity 99.8%; Pred. No. 1.5e-139;  
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DEFINITION Pseudomonas stutzeri intergenic spacer, trna-ile and trna-ala  
genes, strain AER2.5.  
ACCESSION AJ390585  
VERSION AJ390585.1 GI:9844625  
KEYWORDS IGS: intergenic spacer; transfer RNA Ile; transfer RNA-ala;  
trna-ala gene; trna-ile gene.  
SOURCE Pseudomonas stutzeri.  
ORGANISM Pseudomonas stutzeri.  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.  
REFERENCE 1 (bases 1 to 505)  
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasir,A.  
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for

the definition of Pseudomonas stutzeri genomovars and other  
Pseudomonas species  
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
JOURNAL MEDLINE 20393664  
PUBMED 10939670  
REFERENCE 2 (bases 1 to 505)  
AUTHORS Bannasir,A.  
TITLE Direct Submission  
SUBMITTED (15-DEC-1999) Bannasir A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascheroder Weg 1,  
D-38124 Braunschweig, GERMANY  
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source Location/Qualifiers  
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177. .251  
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QY 481 TAACAGATTGCTTGGGTTATAT 504  
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PST390582  
LOCUS PST390582 505 bp DNA linear BCT 16-AUG-2000

DEFINITION Pseudomonas stutzeri intergenic spacer, tRNA-Ile and tRNA-Ala  
 genes, strain SADN19.  
 ACCESSION AJ390582  
 VERSION AJ390582.1 GI:9844622  
 KEYWORDS IGS; intergenic spacer; transfer RNA Ile; transfer RNA-Ala;  
 tRNA-Ala gene; tRNA-Ile gene.  
 SOURCE Pseudomonas stutzeri.  
 ORGANISM Pseudomonas stutzeri.  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 Pseudomonas.  
 1 (bases 1 to 505)  
 Guasp,C., Moore,E.R., Lalucat,J. and Bennisar,A.  
 Utility of internally transcribed 16S-23S rDNA spacer regions for  
 the definition of Pseudomonas stutzeri genomovars and other  
 Pseudomonas species  
 Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
 JOURNAL MEDLINE  
 PUBMED 20393664  
 REFERENCE 2 (bases 1 to 505)  
 Bennisar,A.  
 Direct Submission  
 Submitted (15-DEC-1999) Bennisar A., Division of Microbiology,  
 National Research Centre for Biotechnology, Mascheroder Weg 1,  
 D-38124 Braunschweig, GERMANY  
 JOURNAL  
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 QY 241 GGCTCCACCATTAAGTCTAGTCCGGAAGCTCAGAAATGAGTGTATACAGGATGAGGT 300  
 Db 242 GGCTCCACCATTAAGTCTAGTCCGGAAGCTCAGAAATGAGTGTATACAGGATGAGAT 301  
 QY 301 TGATTGCTGGTGAACATTTGATCTGCACTTTGCGGACCAACTGCTTTTAAAAATT 360  
 Db 302 TGATTGCTGGTGAACATTTGATCTGCACTTTGCGGACCAACTGCTTTTAAAAATT 361  
 QY 361 TGGGTATGATAGAGTAGACCGATGTTGCTTTTACCTGGCAGCATGTCGGGTCAAGG 420  
 Db 362 TGGGTATGATAGAGTAGACCGATGTTGCTTTTACCTGGCAGCATGTCGGGTCAAGG 421

QY 421 TAAATTTCCGTTCTCTATGCAAAATTTCCGCGAATTCGTTCTTACGTTATAGACAG 480  
 Db 422 TAAATTTCCGTTCTCTATGCAAAATTTCCGCGAATTCGTTCTTACGTTATAGACAG 481  
 QY 481 TAACCAAGATTGCTGGGGTTATAT 504  
 Db 482 TAACCAAGATTGCTGGGGTTATAT 505

RESULT 8  
 PST390583  
 LOCUS Pseudomonas stutzeri intergenic spacer, tRNA-Ile and tRNA-Ala  
 DEFINITION genes, strain SD55473.  
 ACCESSION AJ390583  
 VERSION AJ390583.1 GI:9844623  
 KEYWORDS IGS; intergenic spacer; transfer RNA Ile; transfer RNA-Ala;  
 tRNA-Ala gene; tRNA-Ile gene.  
 SOURCE Pseudomonas stutzeri.  
 ORGANISM Pseudomonas stutzeri.  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 Pseudomonas.  
 1 (bases 1 to 505)  
 Guasp,C., Moore,E.R., Lalucat,J. and Bennisar,A.  
 Utility of internally transcribed 16S-23S rDNA spacer regions for  
 the definition of Pseudomonas stutzeri genomovars and other  
 Pseudomonas species  
 Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
 JOURNAL MEDLINE  
 PUBMED 20393664  
 REFERENCE 2 (bases 1 to 505)  
 Bennisar,A.  
 Direct Submission  
 Submitted (15-DEC-1999) Bennisar A., Division of Microbiology,  
 National Research Centre for Biotechnology, Mascheroder Weg 1,  
 D-38124 Braunschweig, GERMANY  
 JOURNAL  
 FEATURES Location/Qualifiers  
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 /strain="SD55473"  
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 tRNA 93..169  
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 /anticodon=(pos:127..129,aa:Ile)  
 tRNA 177..251  
 /product="tRNA-Ala"  
 /note="codon recognized: GCA"  
 /anticodon=(pos:204..206,aa:Ala)  
 BASE COUNT 121 a 113 c 135 g 136 t  
 ORIGIN

Query Match 99.0%; Score 499.2; DB 1; Length 505;  
 Best Local Similarity 99.4%; Pred. No. 1.4e-138;  
 Matches 501; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCGAAGACACCGGCTTCGTCATAGCTCCACAGTAATGGTCTAGTGGTGGTAGAGCGCA 60  
 Db 2 ATCGAAGACACCGGCTTCGTCATAGCTCCACAGTAATGGTCTAGTGGTGGTAGAGCGCA 61  
 QY 61 GCGATTGGGTTTAGACCGGAGAGTAACGATTGGGTCCTAGCTAGTGGTGGTAGAGCGCA 120  
 Db 62 GCGATTGGGTTTAGACCGGAGAGTAACGATTGGGTCCTAGCTAGTGGTGGTAGAGCGCA 121  
 QY 121 CCCCTGATAAGGTCAGTTCGGCAGTTCGAATCTGCCAGACCCACCAATCGAAGGGGCC 180  
 Db 122 CCCCTGATAAGGTCAGTTCGGCAGTTCGAATCTGCCAGACCCACCAATCGAAGGGGCC 181  
 QY 181 ATAGCTCAGCTGGGAGAGCGCTGCTTTGACGACGAGGTCACGGTTCATCCCGTT 240  
 Db 182 ATAGCTCAGCTGGGAGAGCGCTGCTTTGACGACGAGGTCACGGTTCATCCCGTT 241

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Db 182 ATAGCTCAGCTGGAGAGCGCCTGCTTTGCACGAGGAGGTACGCGTTTCGATCCCGCTT 241
QY 241 GGCTCCACCAATTAACCTAGTCCGCGAAGCTCAGAAATCAGTGTATACCAAGATGAGGT 300
Db 242 GGCTCCACCAATTAACCTAGTCCGCGAAGCTCAGAAATCAGTGTATACCAAGATCAGAT 301
QY 301 TGATTGCTCGGTGGAACATTGATTTCTGGACTTTGCGCCAGAACTGTTCTTTAAAAATT 360
Db 302 TGATCGGCTGGGTGACATTGATTTCTGGACTTTGCGCCAGAACTGTTCTTTAAAAATT 361
QY 361 TGGTATGTGATGAAGTAGACCGATGTTGCTTTTCACTGGCAGCATGTCGCCTCAAGG 420
Db 362 TGGTATGTGATGAAGTAGACCGATGTTGCTTTTCACTGGCAGCATGTCGCCTCAAGG 421
QY 421 TAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAATGTCGTTTCACTGTTATAGACAG 480
Db 422 TAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAATGTCGTTTCACTGTTATAGACAG 481
QY 481 TAACAGATTGCTTGGGGTTATAT 504
Db 482 TAACAGATTGCTTGGGGTTATAT 505

RESULT 9
PST251900
LOCUS
DEFINITION
Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), trna-1le
gene, and trna-Ala gene, strain ATCC 17594.
ACCESSION
AJ251900
VERSION
AJ251900.1 GI:9844588
KEYWORDS
internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer
RNA-1le; trna-Ala gene; trna-1le gene.
SOURCE
Pseudomonas stutzeri.
ORGANISM
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE
1. (bases 1 to 505)
Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.
Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
JOURNAL
MEDLINE
20393664
PUBMED
10939670
REFERENCE
2 (bases 1 to 505)
Bannasar,A.
Direct Submission
Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
LOCATION/Qualifiers
1. .505
/organism="Pseudomonas stutzeri"
/strain="ATCC 17594"
/db_xref="taxon:316"
/note="PCR-amplified rDNA"
misc_feature
1. .505
/note="internal transcribed spacer 1, ITS1"
trna
93..169
/product="trna-1le"
/note="codon recognized: AUC"
/anticodon=(pos:127..129,aa:Ile)
177..251
/product="trna-Ala"
/note="codon recognized: GCA"
/anticodon=(pos:204..206,aa:Ala)
134 g 136 t

BASE COUNT 121 a 114 c 134 g 136 t
ORIGIN

Query Match 97.1%; Score 489.6; DB 1; Length 505;
Best Local Similarity 98.2%; Pred. No. 1.1e-135;
Matches 495; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 1 ATCGAAGACACCGCTTCGCTATAAGCTCCACACAGAAATGCTTGATTCACCTCCGAAAG 60
Db 2 ATCGAAGACACCGCTTCGCTATAAGCTCCACACAGAAATGCTTGATTCACCTCCGAAAG 61
QY 61 GCGATTGGGTTTAGACCCGAGAGTAAGATTTGGTCTGTAGCTCAGTTGGTTAGAGCCGA 120
Db 62 GCGATTGGGTTTAGACCCGAGAGTAAGATTTGGTCTGTAGCTCAGTTGGTTAGAGCCGA 121
QY 121 CCCGTGATAAGGTTGAGTTCGGCAGTTGCAATCTGCCAGACCCACCAATCGAAGGGGCC 180
Db 122 CCCGTGATAAGGTTGAGTTCGGCAGTTGCAATCTGCCAGACCCACCAATCGAAGGGGCC 181
QY 181 ATAGCTCAGCTGGGAGAGCGCTGCTTTGCACGAGGAGGTACGCGTTTCGATCCCGCTT 240
Db 182 ATAGCTCAGCTGGGAGAGCGCTGCTTTGCACGAGGAGGTACGCGTTTCGATCCCGCTT 241
QY 241 GGCTCCACCAATTAACCTAGTCCGCGAAGCTCAGAAATGAGTGTATACCAAGATGAGGT 300
Db 242 GGCTCCACCAATTAACCTAGTCCGCGAAGCTCAGAAATGAGTGTATACCAAGATGAGAT 301
QY 301 TGATTGCTCGGTGGAACATTGATTTCTGGACTTTGCGCCAGAACTGTTCTTTAAAAATT 360
Db 302 TGATCGGCTGGGTGACATTGATTTCTGGACTTTGCGCCAGAACTGTTCTTTAAAAATT 361
QY 361 TGGTATGTGATGAAGTAGACCGATGTTGCTTTTCACTGGCAGCATGTCGCCTCAAGG 420
Db 362 TGGTATGTGATGAAGTAGACCGATGTTGCTTTTCACTGGCAGCATGTCGCCTCAAGG 421
QY 421 TAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAATGTCGTTTCACTGTTATAGACAG 480
Db 422 TAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAATGTCGTTTCACTGTTATAGACAG 481
QY 481 TAACAGATTGCTTGGGGTTATAT 504
Db 482 TAACAGATTGCTTGGGGTTATAT 505

RESULT 10
PST251908
LOCUS
DEFINITION
Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), trna-1le
and trna-Ala, strain DNSP21.
ACCESSION
AJ251908
VERSION
AJ251908.1 GI:9844596
KEYWORDS
internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer
RNA-1le; trna-Ala; trna-1le.
SOURCE
Pseudomonas stutzeri.
ORGANISM
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE
1. (bases 1 to 506)
Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.
Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
JOURNAL
MEDLINE
20393664
PUBMED
10939670
REFERENCE
2 (bases 1 to 506)
Bannasar,A.
Direct Submission
Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
LOCATION/Qualifiers
1. .506
/organism="Pseudomonas stutzeri"
/strain="DNSP21"
/db_xref="taxon:316"
/note="PCR-amplified rDNA"
1. .506
/note="internal transcribed spacer 1, ITS1"
93..169
misc_feature
trna

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trna /product="trna-ile"  
/note="codon recognized: AUC"  
/anticodon=(pos:127..129,aa:ile)  
177..251  
/product="trna-Ala"  
/note="codon recognized: GCA"  
/anticodon=(pos:204..206,aa:Ala)  
BASE COUNT 121 a 113 c 136 g 136 t  
ORIGIN

Query Match 96.5%; Score 486.6; DB 1; Length 506;  
Best Local Similarity 99.0%; Pred. No. 8.4e-135;  
Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Db 2 ATCCAGACACCGGCTTCATAGCTCCACAGCAATTCGATTCACCTTCGGAAG 61  
|||||

QY 61 GCGATTGGGTTAGACCGGAGAGTAACGATTGGGTCCTAGCTCAGTTGGTTAGAGCGCA 120  
|||||  
Db 62 GCGATTGGGTTAGACCGGAGAGTAACGATTGGGTCCTAGCTCAGTTGGTTAGAGCGCA 121  
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QY 121 CCCCTGATAAGGTGAGGTGCGCAGTTCGAATCTCCACAGACCCACCAATCGAAGGGCC 180  
|||||  
Db 122 CCCCTGATAAGGTGAGGTGCGCAGTTCGAATCTCCACAGACCCACCAATCGAAGGGCC 181  
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QY 181 ATAGCTCAGTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGCGGTTTCGATCCCGCTT 240  
|||||  
Db 182 ATAGCTCAGTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGCGGTTTCGATCCCGCTT 241  
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QY 241 GGCCTCCACCATTAACCTAGTCCGCGAAAGCTCAGAAATGAGTTTACCAGGATGA-GG 299  
|||||  
Db 242 GGCCTCCACCATTAACCTAGTCCGCGAAAGCTCAGAAATGAGTTTACCAGGATGA-GG 301  
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QY 300 TTGATTGCTGGGTTGAACATTCGATTCGGACTTTCCGCCAGAACTGTTCTTTAAAAAT 359  
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Db 482 GTAACCAAGATTCGTTGGGGTTATAT 506  
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RESULT 11  
PST390588 506 bp DNA linear BCT 16-AUG-2000  
LOCUS  
DEFINITION  
Pseudomonas stutzeri intergenic spacer, trna-ile and trna-Ala  
genes, strain JDA.  
ACCESSION  
AJ390588  
VERSION  
IGS; intergenic spacer; transfer RNA ile; transfer RNA-Ala;  
trna-Ala gene; trna-ile gene.  
KEYWORDS  
Pseudomonas stutzeri.  
SOURCE  
Pseudomonas stutzeri.  
ORGANISM  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.  
REFERENCE  
1 (bases 1 to 506)  
Guasp,C., Moore,E.R., Lalucat,J. and Bennasar,A.  
AUTHORS  
TITLE  
Utility of internally transcribed 16S-23S rDNA spacer regions for  
the definition of Pseudomonas stutzeri genomovars and other  
Pseudomonas species  
JOURNAL  
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
MEDLINE  
20393664  
PUBMED  
10939670  
REFERENCE  
2 (bases 1 to 506)

Authors  
Bennasar, A.  
Direct Submission  
Submitted (15-DEC-1999) Bennasar A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascheroder Weg 1,  
D-38124 Braunschweig, GERMANY  
Location/Qualifiers  
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1..506  
/organism="Pseudomonas stutzeri"  
/strain="JDA"  
/db\_xref="taxon:316"  
misc\_feature  
1..506  
/note="intergenic spacer"  
93..169  
trna  
/product="trna-ile"  
/note="codon recognized: AUC"  
/anticodon=(pos:127..129,aa:ile)  
177..251  
trna  
/product="trna-Ala"  
/note="codon recognized: GCA"  
/anticodon=(pos:204..206,aa:Ala)  
BASE COUNT 122 a 113 c 136 g 135 t  
ORIGIN

Query Match 95.9%; Score 483.4; DB 1; Length 506;  
Best Local Similarity 98.6%; Pred. No. 7.6e-134;  
Matches 498; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Db 2 ATCCAGACACCGGCTTCATAGCTCCACAGCAATTCGATTCACCTTCGGAAG 61  
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QY 61 GCGATTGGGTTAGACCGGAGAGTAACGATTGGGTCCTAGCTCAGTTGGTTAGAGCGCA 120  
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Db 62 GCGATTGGGTTAGACCGGAGAGTAACGATTGGGTCCTAGCTCAGTTGGTTAGAGCGCA 121  
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QY 121 CCCCTGATAAGGTGAGGTGCGCAGTTCGAATCTCCACAGACCCACCAATCGAAGGGCC 180  
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Db 122 CCCCTGATAAGGTGAGGTGCGCAGTTCGAATCTCCACAGACCCACCAATCGAAGGGCC 181  
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QY 181 ATAGCTCAGTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGCGGTTTCGATCCCGCTT 240  
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Db 182 ATAGCTCAGTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGCGGTTTCGATCCCGCTT 241  
|||||

QY 241 GGCCTCCACCATTAACCTAGTCCGCGAAAGCTCAGAAATGAGTTTACCAGGATGA-GG 299  
|||||  
Db 242 GGCCTCCACCATTAACCTAGTCCGCGAAAGCTCAGAAATGAGTTTACCAGGATGA-GG 301  
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QY 300 TTGATTGCTGGGTTGAACATTCGATTCGGACTTTCCGCCAGAACTGTTCTTTAAAAAT 359  
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Db 302 TTGATTGCTGGGTTGAACATTCGATTCGGACTTTCCGCCAGAACTGTTCTTTAAAAAT 361  
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QY 360 TTGGGTATGTGATAGAGTAGACCGATGTTGCTTCTACTGGCAGCATCTCGCGTCAAG 419  
|||||  
Db 362 TTGGGTATGTGATAGAGTAGACCGATGTTGCTTCTACTGGCAGCATCTCGCGTCAAG 421  
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QY 420 GTAAATTTGCGGTTCCTCTATGCAAAATTTCCGCCGAATGCTGCTTCACGTTATAGACA 479  
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Db 422 GTAAATTTGCGGTTCCTCTATGCAAAATTTCCGCCGAATGCTGCTTCACGTTATAGACA 481  
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QY 480 GTAACCAAGATTCGTTGGGGTTATAT 504  
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Db 482 GTAACCAAGATTCGTTGGGGTTATAT 506  
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RESULT 12  
PST251905 528 bp DNA linear BCT 16-AUG-2000  
LOCUS  
DEFINITION  
Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), trna-ile  
and trna-Ala, strain AN11.  
ACCESSION  
AJ251905  
VERSION  
AJ251905.1 GI:9844593  
KEYWORDS  
Internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer  
RNA-ile; trna-Ala; trna-ile.

Qy	454	CGAATGTCGTCTTACAGTTATAGACAGTAACACAGATTCGTTGGGGTTATAT	504
Db	478	CGAATGTCGTCTTACAGTTATAGACAGTAACACAGATTCGTTGGGGTTATAT	528
RESULT 13			
PST251903			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
misc_feature			
tRNA			
tRNA			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
Qy	1	ATCGAAGACACCGGCTTCGTTCATAAGCTCCACACGAAATTCCTTGATTCACCTGCGAAAG	60
Db	2	ATCGAAGACTCAGCGCTTCCTTCAAGAGTCCACACGAAATTCCTTGATTCACCTGCGAAAG	61
Qy	61	GCgATTGGGTTTACGCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA	120
Db	62	GCgATTGGGTTTACGCCGAGAGAGAGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA	121
Qy	121	CCCTGTATAGGTGAGGTGCGGAGTTCGAATCTGCCACACCCACCAA-----	169
Db	122	CCCTGTATAGGTGAGGTGCGGAGTTCGAATCTGCCACACCCACCAA-----	181
Qy	170	-----TCGAAGGGGCCATAGCTCAGCTGGGAGAGCGCTTCGCTTGCACGCAG	216
Db	182	TGTTGGCGGATCTGTAGATGTTGGGCGCATAGCTCAGCTGGGAGAGCGCTTCGCTTGCACGCAG	241
Qy	217	GAGGTGAGCGGTTTCGATCCCGCTTGCGTCCACCATTAACATC--TAGTGCAGCGCAAGCTCA	274

Db 242 GAGGTCAGCGGTTCCGATCCCGCTTGGCTCCACCATTAACTCGAAATAATCGCTGAAAGCTCA 301

QY 275 GAAATGAGTGTATACAGAGAGAGGTTGATTGCGCTGGGTTGAAACATTAATTCCTGGACTT 334

Db 302 GAAATGAGTGTATACAGAGAGAGGTTGATTGCGCTGGGTTGAAACATTAATTCCTGGACTT 357

QY 335 TCGCCGAGAACTGTTCTTTAAATAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 393

Db 358 TCGCCGAGAACTGTTCTTTAAATAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 417

QY 394 TTTCACTGGCAGCATGTCGCTCAAGTAAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 453

Db 418 TTTCACTGGTGTATTAATCAAGTCAAGGTAAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 477

QY 454 CGAATGTCGTTTACAGGATGAGTTGATTCGCTGGGTTGAACATTAATTCCTGGACTT 504

Db 478 CGAATGTCGTTTACAGGATGAGTTGATTCGCTGGGTTGAACATTAATTCCTGGACTT 528

RESULT 14

PST390589

LOCUS

DEFINITION

Pseudomonas stutzeri intergenic spacer, trna-ile and trna-Ala

genes, strain P11.

ACCESSION

AJ390589

VERSION

1

KEYWORDS

IGS; intergenic spacer; transfer RNA Ile; transfer RNA-Ala;

trna-Ala gene; trna-ile gene.

SOURCE

Pseudomonas stutzeri.

ORGANISM

Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

Pseudomonas.

REFERENCE

1 (bases 1 to 528)

Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.

Utility of internally transcribed 16S-23S rDNA spacer regions for

the definition of Pseudomonas stutzeri genomovars and other

Pseudomonas species

Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)

20393664

PUBLISHED

10939670

REFERENCE

2 (bases 1 to 528)

Bannasar,A.

Direct Submission

Submitted (15-DEC-1999) Bannasar A., Division of Microbiology,

National Research Centre for Biotechnology, Mascheroder Weg 1,

D-38124 Braunschweig, GERMANY

LOCATION/Qualifiers

1. .528

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/strain="P11"

/db\_xref="taxon:316"

/note="intergenic spacer"

1. .528

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/note="codon recognized: AUC"

/anticodon="(pos:127..129,aa:Ile)

201..275

/product="trna-Ala"

/note="codon recognized: GCA"

/anticodon="(pos:228..230,aa:Ala)

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BASE COUNT

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ORIGIN

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Best Local Similarity 84.0%; Pred. No.1.3e-91;

Matches 446; Conservative 0; Mismatches 54; Indels 31; Gaps 4;

QY 1 ATCGAAGACACCGGTTCTGATAGAGTCCACAGCAATTCGTTGATTCACCTGCGAAG 60

Db 2 ATCGAAGACCTCAGCTTCTATAGAGTCCACAGCAATTCGTTGATTCACCTAGCGAAA 61

QY 61 GCGATTGGGTTTAGACCCGAGAGTAACGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA 120

Db 62 GCATTTGGGTTTCGCCGAGAGAGAGGATTTGGGTTCTGTAGCTCAGTTGTTAGAGCGCA 121

QY 121 CCCTGATTAAGGTGAGTGGGAGTTCGATTCGATTCGCCAGACCCACCA- 169

Db 122 CCCTGATTAAGGTGAGTGGGAGTTCGATTCGATTCGCCAGACCCACCAATTTGTCATGGGA 181

QY 170 -----TCGAAGGGGCGCATAGCTCAGCTGAGGAGGCGCTGCTTCACGCGAG 216

Db 182 TGTGGCCGATCTGTAGATGGGCGCATAGCTCAGCTGAGGAGGCGCTGCTTCACGCGAG 241

QY 217 GAGTTCAGCGGTTGATTCGCCGCTGGGTCACCATTAATTC- 274

Db 242 GAGTTCAGCGGTTGATTCGCCGCTGGGTCACCATTAATTCGAAATTCGTTGAAAGCTCA 301

QY 275 GAAATGAGTGTTCACAGGATGAGTTGATTCGCTGGGTTGAACATTAATTCCTGGACTT 334

Db 302 GAAATGAGTGTTCACAGGATGAGTTGATTCGCTGGGTTGAACATTAATTCCTGGACTT 357

QY 335 TCGCCGAGAACTGTTCTTTAAATAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 393

Db 358 TCGCCGAGAACTGTTCTTTAAATAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 417

QY 394 TTTCACTGGCAGCATGTCGCTCAAGTAAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 453

Db 418 TTTCACTGGTGTATTAATCAAGTCAAGGTAAATTTGGGTATGTATGATAGAGTAGA-CCGATGTGTTC 477

QY 454 CGAATGTCGTTTACAGGATGAGTTGATTCGCTGGGTTGAACATTAATTCCTGGACTT 504

Db 478 CGAATGTCGTTTACAGGATGAGTTGATTCGCTGGGTTGAACATTAATTCCTGGACTT 528

RESULT 15

PST251904

LOCUS

DEFINITION

Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), trna-ile

and trna-Ala, strain AN10.

ACCESSION

AJ251904

VERSION

1

KEYWORDS

Internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer

RNA-ile; trna-Ala; trna-ile.

SOURCE

Pseudomonas stutzeri.

ORGANISM

Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

Pseudomonas.

REFERENCE

1 (bases 1 to 529)

Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.

Utility of internally transcribed 16S-23S rDNA spacer regions for

the definition of Pseudomonas stutzeri genomovars and other

Pseudomonas species

Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)

20393664

PUBLISHED

10939670

REFERENCE

2 (bases 1 to 529)

Bannasar,A.

Direct Submission

Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,

National Research Centre for Biotechnology, Mascheroder Weg 1,

D-38124 Braunschweig, GERMANY

LOCATION/Qualifiers

1. .529

/organism="Pseudomonas stutzeri"

/strain="AN10"

/db\_xref="taxon:316"

/note="PCR-amplified rDNA"

1. .529

/note="internal transcribed spacer 1, ITS1"

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/product="trna-ile"

/note="codon recognized: AUC"

/anticodon="(pos:127..129,aa:Ile)

201..275

/product="trna-Ala"

misc\_feature

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trna

93..169

trna

201..275

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 19:23:36 ; Search time 119.347 Seconds  
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Title: US-09-931-486-113

Perfect score: 504

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Scoring table: IDENTITY\_NUC  
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	504	100.0	504	17	AAT11844
2	265.4	52.7	499	17	AAT11845
3	249	49.4	520	17	AAT11843
4	225.8	44.8	471	17	AAT11842
5	205.2	40.7	468	17	AAT11846
6	184.4	36.6	588	22	AAI69774
7	117.2	23.3	664	12	AAQ14106
8	110.6	21.9	1396	22	AAH55089
9	110.6	21.9	2839	22	AAH54998

10	110.6	21.9	3444	22	AAH54992
11	110.6	21.9	4429	22	AAH54300
12	109.8	21.8	400	18	AAV78022
13	108.6	21.5	603	12	AAQ14102
14	108.6	21.5	640681	24	ABA92787
15	108.4	21.5	20844	21	AAA81460
16	108.4	21.5	172325	21	AAF21613
17	108.4	21.5	349980	21	AAF21544
18	108.4	21.5	349980	21	AAF21607
19	108.4	21.5	349980	21	AAF21611
20	108.4	21.5	349980	21	AAF21612
21	108.4	21.5	837096	21	AAA81489
22	108.4	21.5	1437668	21	AAA81490
23	108.2	21.5	400	18	AAV77902
24	108.2	21.5	1311	18	AAV77852
25	107.2	21.3	400	18	AAV77984
26	107	21.2	335	12	AAQ14103
27	102.8	20.4	808	17	AAT11889
28	102.8	20.4	808	17	AAT11890
29	102.8	20.4	809	17	AAT11891
30	102.6	20.4	351	18	AAV78405
31	97.8	19.4	549	12	AAQ14109
32	97	19.2	498	12	AAQ14107
33	97	19.2	269223	22	AAF28554
34	95	18.8	349980	22	AAH64966
35	94.2	18.7	343	18	AAV78492
36	93.6	18.6	400	18	AAV77919
37	91.8	18.2	243	23	AA548781
38	91.4	18.1	470	17	AAT11898
39	91.2	18.1	255	23	AA548800
40	91.2	18.1	255	23	AA548825
41	91.2	18.1	255	23	AA548838
42	91.2	18.1	255	23	AA548846
43	91.2	18.1	255	23	AA548854
44	91.2	18.1	255	23	AA548877
45	91.2	18.1	255	23	AA548882

#### ALIGNMENTS

RESULT 1  
AAT11844  
ID AAT11844 standard; DNA; 504 BP.  
XX AAT11844;  
AC AAT11844;  
XX  
DT 03-SEP-1996 (first entry)  
XX  
DE P. stutzeri LMG 2333 16S-23S rRNA spacer region.  
XX  
KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.  
XX  
OS Pseudomonas stutzeri.  
XX  
PN WO9600298-A1.  
XX  
PD 04-JAN-1996.  
XX  
PF 23-JUN-1995; 95WO-EP02452.  
XX  
PR 07-APR-1995; 95EP-0870032.  
XX  
PR 24-JUN-1994; 94EP-0870106.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Jannes G, Rossau R, Van Heuverswyn H;  
XX  
DR WPT; 1996-068882/07.  
XX  
PT Novel hybridisation assay for the detection of eubacteria - esp

S. epidermidis gen  
S. epidermidis gen  
Staphylococcus aur  
N.gonorrhoeae stra  
Buchnera sp. genom  
N. meningitidis pa  
Neisseria meningit  
Neisseria meningit  
Neisseria meningit  
Neisseria meningit  
N. meningitidis pa  
N. meningitidis B  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur  
N.gonorrhoeae stra  
Brucella melitensi  
Brucella suis NIDO  
Brucella abortus  
Staphylococcus aur  
Staphylococcus aur  
M.nonliquefaciens  
B.catarhalis stra  
Genomic fragment #  
C glutamicum codin  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur  
Yersinia enterocol  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur  
Staphylococcus aur

PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX  
 PS Claim 2; Fig 38; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT3401.1-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *stutzeri* LMG 2333.  
 XX  
 SQ Sequence 504 BP; 119 A; 111 C; 137 G; 137 T; 0 other;  
 Query Match 100.0%; Score 504; DB 17; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-163;  
 Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATCGAAGACACCGGCTTCGTCATTAAGCTCCACACGAAATTCCTGATTCACCTTCGGAAG 60  
 DB 1 ATCGAAGACACCGGCTTCGTCATTAAGCTCCACACGAAATTCCTGATTCACCTTCGGAAG 60  
 QY 61 GCGATTGGTTAGACCCGAGAGTAACGATGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
 DB 61 GCGATTGGTTAGACCCGAGAGTAACGATGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
 QY 121 CCCCTGATAAGGTTAGGTCGGCAGTTGCAATCTGCCAGACCCACCAATCGAAGGGCC 180  
 DB 121 CCCCTGATAAGGTTAGGTCGGCAGTTGCAATCTGCCAGACCCACCAATCGAAGGGCC 180  
 QY 181 ATAGCTCAGCTGGGAGAGCGCTCTGTTGACGAGGAGGTTCAGCGTTCGATCCCGCTT 240  
 DB 181 ATAGCTCAGCTGGGAGAGCGCTCTGTTGACGAGGAGGTTCAGCGTTCGATCCCGCTT 240  
 QY 241 GGCTCCACCAATTAAGTCTAGTGCAGAAAGCTCAGAAATGAGTTTACCAAGATGAGGT 300  
 DB 241 GGCTCCACCAATTAAGTCTAGTGCAGAAAGCTCAGAAATGAGTTTACCAAGATGAGGT 300  
 QY 301 TGATTGCTGGTTGAACATTGATTTCTGGACTTTGCGCCAGAACTGCTCTTTAAATAAT 360  
 DB 301 TGATTGCTGGTTGAACATTGATTTCTGGACTTTGCGCCAGAACTGCTCTTTAAATAAT 360  
 QY 361 TGGTATGCTGATAGAAGTAGACCGATGTTGCTTTTCACTGGCAGCATGTCGCTCAAGG 420  
 DB 361 TGGTATGCTGATAGAAGTAGACCGATGTTGCTTTTCACTGGCAGCATGTCGCTCAAGG 420  
 QY 421 TAAATTTGCTGTTCTCTATGCAAAATTTTCGGCGAATGTCGTTTACGTTATAGACAG 480  
 DB 421 TAAATTTGCTGTTCTCTATGCAAAATTTTCGGCGAATGTCGTTTACGTTATAGACAG 480  
 QY 481 TAACACGATTCTGGGGTTATAT 504  
 DB 481 TAACACGATTCTGGGGTTATAT 504  
 RESULT 2  
 AAT11845  
 ID AAT11845 standard; DNA; 499 BP.  
 XX  
 AC AAT11845;  
 XX  
 DT 03-SEP-1996 (first entry)  
 XX  
 DE *P. alcaligenes* LMG 1224 16S-23S rRNA spacer region.  
 XX  
 KW Probe; detection; identification; microorganism; amplify;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX  
 OS *Pseudomonas* *alcaligenes*.  
 XX

PN WO9600298-A1.  
 XX  
 PD 04-JAN-1996.  
 XX  
 PF 23-JUN-1995; 95WO-EP02452.  
 XX  
 PR 07-APR-1995; 95EP-0870032.  
 PR 24-JUN-1994; 94EP-0870106.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Jannes G. Rossau R. Van Heulewyn H.  
 XX  
 DR WPI; 1996-068882/07.  
 XX  
 PT Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 XX  
 XX Claim 2; Fig 39; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT3401.1-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *alcaligenes* LMG 1224.  
 XX  
 SQ Sequence 499 BP; 123 A; 109 C; 130 G; 137 T; 0 other;  
 Query Match 52.7%; Score 265.4; DB 17; Length 499;  
 Best Local Similarity 78.5%; Pred. No. 4.4e-81;  
 Matches 412; Conservative 0; Mismatches 66; Indels 47; Gaps 6;  
 QY 1 ATCGAAGACACCGGCTTCGTCATTAAGCTCCACACGAAATTCCTGATTCACCTTCGGAAG 60  
 DB 1 ATCGAAGACACCGGCTTCGTCATTAAGCTCCACACGAAATTCCTGATTCACCTTCGGAAG 60  
 QY 61 GCGATTGGTTAGACCCGAGAGTAACGATGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
 DB 61 GCGATTGGTTAGACCCGAGAGTAACGATGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
 QY 121 CCCCTGATAAGGTTAGGTCGGCAGTTGCAATCTGCCAGACCCACCAATTCGCGGATG 172  
 DB 121 CCCCTGATAAGGTTAGGTCGGCAGTTGCAATCTGCCAGACCCACCAATTCGCGGATG 180  
 QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTTCCTTTCACCGCAGAGGT 221  
 DB 181 GCCAGTGTCAATGGGCGCATAGCTCAGCTGGGAGAGCGCTTCCTTTCACCGCAGAGGT 240  
 QY 222 CAGCGGTTTCGATCCGCTTGGCTCCACCATTAACCTCTAG-TCGCCGAAGCTCAGAAATG 280  
 DB 241 CAGGATTTCGATCTCTTGGCTCCACCATCACTCAGATCGCTGAAGCTCAGAAATG 300  
 QY 281 AGTGTTCACAGGATGAGGTTGATTCGCTGGTTGAACATGATTTCTGGACTTTGCGCC 340  
 DB 301 AACATT-----GGTAGTCAATGTTGATTTCTGGTCTTTCGCTTCGCGCC 339  
 QY 341 AGAAGTGTCTTTAAATTTGGGTATGTATAGAGTAGACCGATGTTGCTTTCCTTCACT 400  
 DB 340 AGAAGTGTCTTTAAATTTGGGTATGTATAGAGTAGACCGATGTTGCTTTCCTTCACT 395  
 QY 401 GGCAGCATGTCGCGTCAAGGTAATAATTTGCGTGTGTTCTCTATGCAAAATTTTCGGCGAATGT 460  
 DB 396 CTGCACGTTGTTAATCAAGGCAAAATTTGCGAGTTC-AAGCGGATTTTCGCGCAATGT 454  
 QY 461 CGCTTTCACGTTA-TAGACAGTAACGATGCTTGGGGTTATAT 504  
 DB 455 CGCTTTCACGTTACGAATCTATACACGAGATTGCTTGGGGTTATAT 499

## RESULT 3

AAT11843  
 ID AAT11843 standard; DNA; 520 BP.  
 XX  
 AC AAT11843;  
 XX  
 DT 03-SEP-1996 (first entry)  
 XX  
 XX  
 DE P. psedocaligenes LMG 1225 16S-23S rRNA spacer region.  
 XX  
 KW Probe; detection; identification; microorganism; amplify;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX  
 OS Pseudomonas pseudoalcaligenes.  
 XX  
 PN W09600298-A1.  
 XX  
 PD 04-JAN-1996.  
 XX  
 PF 23-JUN-1995; 95WO-EP02452.  
 XX  
 PR 07-APR-1995; 95EP-0870032.  
 PR 24-JUN-1994; 94EP-0870106.  
 XX  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Jannes G, Rossau R, Van Heuverswyn H.  
 XX  
 DR WPI; 1996-068882/07.  
 XX  
 XX Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 PT  
 XX  
 PS Claim 2; Fig 37; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from Pseudomonas  
 CC pseudoalcaligenes LMG 1225.  
 CC  
 XX  
 SQ Sequence 520 BP; 126 A; 109 C; 134 G; 151 T; 0 other;

Query Match 49.4%; Score 249; DB 17; Length 520;  
 Best Local Similarity 74.4%; Pred. No. 2.1e-75;  
 Matches 392; Conservative 0; Mismatches 105; Indels 30; Gaps 5;

Qy 1 ATCGAAGACACGGGCTTCGTATAGCTCCACAGCAATGCTGATTCACCTGCGAAG 60  
 Db 1 ATCGAAGACATCAGCTTCTTATAGTATCCACAGCAATGCTGATTCACCTGCGAAG 60  
 Qy 61 CGGATTGGTTAGACCGAGAGTAACGATGGGCTCTAGCTCAGTGGTTAGAGCGCA 120  
 Db 61 AATGCTGTAAACGACCGACCGTGTATA-----GGTCTAGTCTAGTGGTTAGAGCGCA 114  
 Qy 121 CCCCTGATAAGGGTGGAGTCGGCAGTTCGAATCTGCCAGACCCACCAATCG-----172  
 Db 115 CCCCTGATAAGGGTGGAGTCGGCAGTTCGAATCTGCCAGACCTACCAATGCTTGGTCG 174  
 Qy 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGTGAG 224  
 Db 175 AGAAGATACGGGGCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGTGAG 234  
 Qy 225 CGGTCGATCCCGCTTGGCTCCACATTAAGTCTAGTCCGCGAAGAGCTCAGAAATGAGTG 284  
 Db 235 CGGTCGATCCCGCTTGGCTCCACACATCTCTCGTGTGGGTGAGTGTAAAGAGTCA 294  
 Qy 285 TTACCAGGATGAGTGTGATTGCTGGGTGGAACATGATTCTTGGACTTT-----GCG 338

## RESULT 4

AAT11842  
 ID AAT11842 standard; DNA; 471 BP.  
 XX  
 AC AAT11842;  
 XX  
 DT 03-SEP-1996 (first entry)  
 XX  
 DE P. aeruginosa UZG 5669 16S-23S rRNA spacer region.  
 XX  
 KW Probe; detection; identification; microorganism; amplify;  
 KW 16S-23S rRNA spacer region; respiratory tract; universal;  
 KW species-specific; ss.  
 XX  
 OS Pseudomonas aeruginosa.  
 XX  
 PN W09600298-A1.  
 XX  
 PD 04-JAN-1996.  
 XX  
 PF 23-JUN-1995; 95WO-EP02452.  
 XX  
 PR 07-APR-1995; 95EP-0870032.  
 PR 24-JUN-1994; 94EP-0870106.  
 XX  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Jannes G, Rossau R, Van Heuverswyn H.  
 XX  
 DR WPI; 1996-068882/07.  
 XX  
 XX Novel hybridisation assay for the detection of eubacteria - esp  
 PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
 PT  
 XX  
 PS Claim 2; Fig 36; 248pp; English.  
 XX  
 CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
 CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from Pseudomonas  
 CC aeruginosa UZG 5669.  
 CC  
 XX  
 SQ Sequence 471 BP; 116 A; 103 C; 120 G; 132 T; 0 other;

Query Match 44.8%; Score 225.8; DB 17; Length 471;  
 Best Local Similarity 75.1%; Pred. No. 2e-67;  
 Matches 396; Conservative 0; Mismatches 52; Indels 79; Gaps 6;

Qy 1 ATCGAAGACACCGGCTTCGTATAGCTCCACAGCAATGCTGATTCACCTGCGAAG 60  
 Db 1 ATCGAAGATCCCGGCTTCGTATAGCTCCACAGCAATGCTGATTCACCTGCTAG-- 58  
 Qy 61 CGGATTGGTTAGACCCCGAGAGTAACGATTGGGCTCTAGCTCAGTGTGTTAGAGCGCA 120

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Db 59 -----ACGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA 93
QY 121 CCCTGATGAAGGTGAGGTGCGCAGTTTGAATCTGCCAGAGCCACCAATCG----- 172
Db 94 CCCTGATGAAGGTGAGGTGCGCAGTTTGAATCTGCCAGAGCCACCAATTTGTTGGTGTG 153
QY 173 -----AAGGGCCATAGCTCAGCTGAGTGGGAGAGCGCCTGCTTTGCACGCAGGA 218
Db 154 CTGCGTGATCCGATACGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGCAGGA 213
QY 219 GGTACAGCGGTTCGATCCCGCTTGGCTCCACCAATTAACCTCTAGTCCGCGAAAGCTCAGAAA 278
Db 214 GGTACAGAGTTCGATCCCTTGGCTCCACCAATTAACCTCTAGTCCGCGAAAGCTCAGAAA 273
QY 279 TGAGTGTTTTACCAGGATGAGGTTGATTGCTGGGTTGAACATTGATTCTTGACATTTGGC 338
Db 274 TGAATGTT-----CGTGGATGAACATTGATTCTTGCTGCTTTGCA 312
QY 339 CCAGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAAGT-AGACCGGATGTGTTGCTTTC 397
Db 313 CCAGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAAGTGAAGTCTGATCTCTTTC 372
QY 398 ACTGSCACCATGTCGCGTCAAGGTAATAATTTGGCGTGTCTCTATGCAAAATTTTCGGCGAA 457
Db 373 ACTGCTGATCATCAAGTCAAGGTAATAATTTGGCGATTC-AAGCGCGAATTTTCGGCGAA 431
QY 458 TGTCGCTCTTACGTTATAGACAGTAACACGATTTGCTGGGTTTATAT 504
Db 432 TGTCGCTCTTACAGTA-----TAACAGGATGCTTGGGGTTTATAT 471

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## RESULT 5

AAI11846

ID AAI11846 standard; DNA; 468 BP.

XX AC AAI11846;

DT 03-SEP-1996 (first entry)

XX DE P. putida LMG 2232 16S-23S rRNA spacer region.

XX KW Probe; detection; identification; microorganism; amplify;

KW 16S-23S rRNA spacer region; respiratory tract; universal;

XX KW species-specific; ss.

XX OS Pseudomonas putida.

XX PN WO9600298-A1.

XX PD 04-JAN-1996.

XX PF 23-JUN-1995; 95WO-EP02452.

XX PR 07-APR-1995; 95EP-0870032.

XX PR 24-JUN-1994; 94EP-0870106.

XX XX (INNO-) INNOGENETICS NV.

XX PI Jannes G, Rossau R, Van Heuverswyn H;

XX XX WPI; 1996-068882/07.

XX PT Novel hybridisation assay for the detection of eubacteria - esp

XX PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region

XX PS Claim 2; Fig 40; 248pp; English.

XX CC The sequences given in AAI11791-857 represent the 16S-23S rRNA spacer  
 CC regions derived from various microorganisms. These sequences were  
 CC used in the method of the invention for the detection and identification  
 CC of at least one or more microorganisms. The method comprises amplifying  
 CC the 16S-23S rRNA spacer region and hybridising one or more of the probes

CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC putida LMG 2232.

XX SQ Sequence 468 BP; 117 A; 101 C; 117 G; 133 T; 0 other;

## Query Match

Best Local Similarity 40.7%; Score 205.2; DB 17; Length 468;  
 Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;

```

QY 1 ATCAGAGACACACGGCTTCGTCATAGCTCCACACAGAAATGCTTGATTCTACTTGCACAAAG 60
Db 1 ATCAGAGACATCAGCTGCTCATAGCTCCACACAGAAATGCTTGATTCTCA-TTGAAGAAG 59
QY 61 GCGATTGGSTTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGTTAGAGCGCA 120
Db 60 ACGATTAGGTTAGCAACCTT-----CGATTGGGTCTGTAGCTCAGTTGTTAGAGCGCA 113
QY 121 CCCCTGATAAGGTGAGGTGCGCAGTTCGAATCTGCCAGAGCCACCAA-TCGAAGGGC 179
Db 114 CCCCTGATAAGGTGAGGTGCGCAGTTCGAATCTGCCAGAGCCACCAAATTTGCTGGGCG 173
QY 180 CATAGCTCAGCTGGGAGAGCGCTGTTGACAGCAGGAGTCAAGGTTCCATCCCGCT 239
Db 174 CATAGCTCAGCTGGGAGAGCGCTGCTCCCTGTCACGAGGAGTCAAGGTTCCATCCCGCT 233
QY 240 TGGCTCCACCATTAACCTAGTCTAGTCGCCGAAAGCTCAGAAATAGTCTTTACCAAGGATGAGG 299
Db 234 TGGCTCCACC-----ACCCCGCTTGGCAGTTTGTCAAAAGCTTAGAA 274
QY 300 TTGATTGCTGGGTTGAACATTGATTCTGGACTTTGGCCAGAGAACTGTCTTTAAAAAT 359
Db 275 ATGAATATTCGCGTCGAATATTGATTCTGAACTTT--ATCAGAAATCGTTCTTTAAAAAT 332
QY 360 TTGGGTATGTCATAGAACTAGA-CGGATGCTGTGCTTTTCACTGGCAGCATGTCGGGTCAA 418
Db 333 TTGGGTATGTCATAGAAAGATAGACTGGACAGCACTTTTCACTGGGTGTGTGTTCAAGGTAA 392
QY 419 GGTAAATTTGCGTGTCTTCTATGCAAAATTTTCGGCGAAATGTCGCTCTTCAAGTTATAGAC 478
Db 393 GGTAAATTTGCGTGTCTTCTATGCAAAATTTTCGGCGAAATGTCGCTCTTCAAGTTATAGAC 478
QY 479 AGTAACACAGATTGCTTGGGGTTATAT 504
Db 445 --TAACACAGATTGCTTGGGGTTATAT 468

```

## RESULT 6

AAI69774

ID AAI69774 standard; DNA; 588 BP.

XX AC AAI69774;

XX DT 13-DEC-2001 (first entry)

XX DE 16S/23S rRNA spacer region.

XX KW Bacterium detection; 16S/23S rRNA spacer region; ds.

XX OS Pseudomonas putida.

XX PN JP2001190279-A.

XX XX 17-JUL-2001.

XX PF 13-JAN-2000; 2000JP-0004160.

XX PR 13-JAN-2000; 2000JP-0004160.

XX XX (MITO ) MITSUBISHI JUKOGYO KK.

XX XX WPI; 2001-605311/69.



XX Detection method of Pseudomonas bacteria -  
XX Claim 6; Page 7; 11pp; Japanese.  
XX  
XX The present invention relates to a method for the detection of the  
XX present DNA sequence: the 16S/23S rRNA spacer region of Pseudomonas  
XX putida. The method can be used to detect Pseudomonas bacteria.  
XX  
XX Sequence 588 BP; 147 A; 134 C; 153 G; 149 T; 5 other;  
SQ  
Query Match 36.6%; Score 184.4; DB 22; Length 588;  
Best Local Similarity 70.8%; Pred. No. 4.6e-53;  
Matches 366; Conservative 0; Mismatches 91; Indels 60; Gaps 7;  
QY 1 ATCAAGACACGGCTCGTATAGCTCCACACAGAAATTCGTGATTCACATTCGGAAG 60  
Db ATTCAGACATCAGCCTGCTGATGAGTCCACACAGAAATTCGTGATTCGGAAGA 122  
QY 61 GCGATTGGGTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTAGTTGGTTAGAGCGCA 120  
Db ATTCAGACATTCATATA-----TAGTCTGTAGCTAGTTGGTTAGAGCGCA 168  
QY 121 CCCTGTATAAGGGTGAAGTCGGCAGTTCGAATCTGCCAGACCCACCAATCGAAGGGCC 180  
Db CCCCTGTATAANGGTGAGTGGCAGTTCGAATCTGCCAGACCCACCAATCGAAGGGCC 228  
QY 181 ATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGAGGAGTTCAGCGGTTCGATCCCGCTT 240  
Db ATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGAGGAGTTCAGCGGTTCGATCCCGCTT 288  
QY 241 GGCTCCACCAATTAATCTAGTCGCCGAAAGCTCAGAAATGAGTGTACCAGGATGAGGT 300  
Db GGCTCCACCAATTCGTGTACCTGATCAACTCANAATGAGCATCC----- 337  
QY 301 TGATTGCCGTGGTGAACATTTGTTGCGACTTTGCGCCAGAACTGTTCTTTAAATAAT 360  
Db -----GTCTAATGTTGATTTCTGCGTTTGT-----TCAGATCGTCTTTAAATAAT 383  
QY 361 TGGTATGTGATAGAAGTAGACCGATGTTGCTTCTACTGCACGATGTCGCGTCAAGG 420  
Db CGGATGTGTATAGATATAGACTGAACACCAAG-TTTTCTACTGCTGTGATCAGGCTAAG 442  
QY 421 TAAATTTGCGTGTCT-----CTATGCAAAATTTTGGCGAAATGTCGCTCTC 467  
Db TAAATTTGAGTCTGCTCGAAGAGCAACTTNCGAATTTTGGCGAAATGTCGCTCTC 502  
QY 468 ACGTTATAGACAGTAACAGATTCGTTGGGTTATAT 504  
Db -----TAACACAGATTCGTTGGGTTATAT 532

RESULT 7  
AAQ14106  
ID AAQ14106 standard; DNA; 664 BP.  
XX  
AC AAQ14106;  
XX  
DT 10-JAN-1992 (first entry)  
XX  
XX N.meningitidis NCTC 10025 16S to 23S rRNA gene spacer region.  
XX  
XX rRNA gene; ribosomal RNA; probe; ss.  
XX  
XX Neisseria meningitidis NCTC 10025.  
XX  
XX EP452596-A.  
XX  
XX 23-OCT-1991.  
XX  
XX 18-APR-1990; 90EP-0401054.  
XX  
XX 18-APR-1990; 90EP-0401054.  
PR

XX (INNO-) INNOGENETICS NV SA.  
XX  
XX Rossau R, Van Heuverswijn H;  
XX  
XX WPI; 1991-311940/43.  
XX  
XX Hybridisation probes for detecting non-viral microorganisms -  
XX derived from spacer region between 16S and 23S rRNA genes, for  
XX detecting e.g. BORDETELLA PERTUSSIS, NEISSERIA GONORRHOEA  
XX  
XX Disclosure; Fig 3; 41pp; English.  
XX  
XX This sequence is the non-coding strand of the 16S-23S rRNA gene  
XX spacer region; the 5'-end is proximal to the 16S rRNA gene and the 3'  
XX -end proximal to the 23S rRNA gene. A set of probes was designed  
XX based on this sequence which was specific for N.meningitidis. A kit  
XX is provided for detection of this species using the probes.  
XX  
XX Sequence 664 BP; 235 A; 123 C; 154 G; 152 T; 0 other;  
SQ  
Query Match 23.3%; Score 117.2; DB 12; Length 664;  
Best Local Similarity 82.7%; Pred. No. 8.1e-30;  
Matches 134; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGTCCGAGTTCGAA 151  
Db 100 GGGTTTGTAGCTCAGTTGGTTAGAGCACACGCTTGATAGCGTGGGTCCGAGGTCAAG 159  
QY 152 TCTGCCAGACCCCAATCGAAGGGGCGCATAGCTCAGTGGGAGAGCGCTTGTGCA 211  
Db 160 TCTGCCAGACCCCAAGAGCGGGGCGCATAGCTCAGTGGTGTAGAGCACCTGCTTGA 219  
QY 212 GCGAGAGGTGAGCGGTTCGATCCCGTGGTCCGCTCCACCAATTA 253  
Db 220 AGCAGGGGTGATCGTGGTTCGATCCCGTGGTCCGCTCCACCAATA 261  
RESULT 8  
AAH55089  
ID AAH55089 standard; DNA; 1396 BP.  
XX  
AC AAH55089;  
XX  
XX 03-SEP-2001 (first entry)  
XX  
XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:4453.  
XX  
XX Staphylococcus epidermidis SR1 strain; infection; diagnosis;  
XX vaccination; endocarditis; ds.  
XX  
XX Staphylococcus epidermidis.  
XX  
XX WO200134809-A2.  
XX  
XX 17-MAY-2001.  
XX  
XX 09-NOV-2000; 2000WO-US30782.  
XX  
XX 09-NOV-1999; 99US-0164258.  
XX  
XX (GLAX ) GLAXO GROUP LTD.  
XX  
XX KImmerly WJ;  
XX  
XX WPI; 2001-316495/33.  
XX  
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
XX useful for vaccinating against infections, e.g. endocarditis -  
XX  
XX Claim 8; Page 2187-2188; 2188pp; English.  
XX  
XX AAH52304 to AAH53970 represent nucleic acids (1) encoding polypeptides



Mon Feb 3 16:49:05 2003

us-09-931-486-113.rng

```

PI Kimmerly WJ;
XX
DR WPI; 2001-316495/33.
XX
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
XX
XX Claim 8; Page 2096-2097; 2188pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AG81454 to AG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
XX Sequence 3444 BP; 1203 A; 597 C; 723 G; 921 T; 0 other;
SQ
Query Match 21.9%; Score 110.6; DB 22; Length 3444;
Best Local Similarity 79.7%; Pred. No. 3.7e-27;
Matches 149; Conservative 0; Mismatches 24; Indels 14; Gaps 1;

QY 89 ATTGGGCTGTAGCTCAGTGGTGTAGAGCGCACCCCTGATAAGGGTGAGGTGCGCAGTTC 148
DB 2708 AATGGGCTGTAGCTCAGTGGTGTAGAGCGCACCCCTGATAAGGGTGAGGTGCGTGGTTC 2767

QY 149 GAATCTGCCAGACCCACCAATCGA-----AGGGGCCCATAGCTCAGCTGGG 194
DB 2768 GAGTCCACTTAGGCCACCAATCAATAATTTAAACCTTAGGGGGCTTAGCTCAGCTGGG 2827

QY 195 AGAGCGCTGCTTTGCACGAGGAGGTGAGCGGTTCGATCCGCTTGCCTCCACCATTA 254
DB 2828 AGAGCGCTGCTTTGCACGAGGAGGTGAGCGGTTCGATCCGCTTGCCTCCACCATTA 2887

QY 255 CTCTAGT 261
DB 2888 ATTTTGT 2894

RESULT 11
AAH54300
ID AAH54300 standard; DNA; 4429 BP.
XX
XX AAH54300;
AC
XX
XX 03-SEP-2001 (first entry)
XX
XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:3664.
XX
XX Staphylococcus epidermidis SRI strain; infection; diagnosis;
KW vaccination; endocarditis; ds.
XX
XX Staphylococcus epidermidis.
XX
XX WO200134809-A2.
XX
XX 17-MAY-2001.
XX
XX 09-NOV-2000; 2000WO-US30782.
PF

```

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XX 09-NOV-1999; 99US-0164258.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Kimmerly WJ;
XX
XX WPI; 2001-316495/33.
XX
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
XX
XX Claim 8; Page 1270-1272; 2188pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AG81454 to AG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
XX Sequence 4429 BP; 1327 A; 928 C; 1004 G; 1170 T; 0 other;
SQ
Query Match 21.9%; Score 110.6; DB 22; Length 4429;
Best Local Similarity 79.7%; Pred. No. 4.2e-27;
Matches 149; Conservative 0; Mismatches 24; Indels 14; Gaps 1;

QY 89 ATTGGGCTGTAGCTCAGTGGTGTAGAGCGCACCCCTGATAAGGGTGAGGTGCGCAGTTC 148
DB 2768 AATGGGCTGTAGCTCAGTGGTGTAGAGCGCACCCCTGATAAGGGTGAGGTGCGTGGTTC 2827

QY 149 GAATCTGCCAGACCCACCAATCGA-----AGGGGCCCATAGCTCAGCTGGG 194
DB 2828 GAGTCCACTTAGGCCACCAATCAATAATTTAAACCTTAGGGGGCTTAGCTCAGCTGGG 2887

QY 195 AGAGCGCTGCTTTGCACGAGGAGGTGAGCGGTTCGATCCGCTTGCCTCCACCATTA 254
DB 2888 AGAGCGCTGCTTTGCACGAGGAGGTGAGCGGTTCGATCCGCTTGCCTCCACCATTA 2947

QY 255 CTCTAGT 261
DB 2948 ATTTTGT 2954

RESULT 12
AAV78022
ID AAV78022 standard; DNA; 400 BP.
XX
XX AAV78022;
AC
XX
XX 16-MAR-1999 (first entry)
XX
XX Staphylococcus aureus contig SEQ ID #3711.
XX
XX Computer readable medium; vaccine; S aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome; ds.
XX

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DE	N.gonorrhoae strain NCTC 8375	16S to 23S rRNA gene spacer region
XX	rRNA gene; ribosomal RNA; probe; ss.	
OS	Neisseria gonorrhoeae NCTC 8375.	
XX	EP452596-A.	
PN	23-OCT-1991.	
XX	18-APR-1990; 90EP-0401054.	
PF	18-APR-1990; 90EP-0401054.	
XX	(INNO-) INNOGENETICS NV SA.	
PA	Rosau R, Van Heuverswijn H;	
XX	WPI; 1991-311940/43.	
DR	Hybridisation probes for detecting non-viral microorganisms -	
PT	derived from spacer region between 16S and 23S rRNA genes, for	
PT	detecting e.g. BORDETELLA PERTUSSIS, NEISSERIA GONORRHOAE	
PS	Disclosure; Fig 3; 41pp; English.	
XX	This sequence is the non-coding strand of the 16S-23S rRNA gene	
CC	spacer region; the 5'-end is proximal to the 16S rRNA gene and the	
CC	-end proximal to the 23S rRNA gene. The sequence is very similar	
CC	to the corresponding region in N.gonorrhoae ITM 4367. A set of	
CC	probes was designed based on this sequence which was specific for	
CC	N.gonorrhoae. A kit is provided for detection of N.gonorrhoae	
CC	using the probes.	
XX		
SQ	Sequence 603 BP; 203 A; 104 C; 145 G; 151 T; 0 other;	
Query Match 21.5%; Score 108.6; DB 12; Length 603;		
Best Local Similarity 84.3%; Pred. NO. 7.2e-27;		
Matches 134; Conservative 0; Mismatches 24; Indels 1; Gaps		
QY	92 GGTCGTGTAGCTCAGTTGGTTAGAGCGGACCCCTCATAGGTCGAGTTCGACGTTTCGAA	1
Db		
QY	99 GGGTTTGTAGCTCAGCTGGTTAGACACACGCTTGATTAAGCTGAGTTCGGAGGTTCAAG	1
Db		
QY	152 TCTGCCACGACCCACCAATCGAAGGGGCCATAGCTCAGCTGGGAGACGGCTGCTTGC	21
Db		
QY	159 TCTCTCCACGCCACCAA-GAAGCGGGGCATAGCTCAGTTGGTAGACACCTGCTTGC	21
Db		
QY	212 CGCAGGAGGTCAGCGGTTTCGATCCCGCTTGGCTCCACCA	250
Db		
QY	218 AGCAGGGGTCATCGTTTCGATCCCGTTGGCTCCACCA	256
Db		
RESULT 14		
ABR92787	ID ABA92787 standard; DNA; 640681 BP.	
XX	ABA92787;	
AC	27-MAR-2002 (first entry)	
DT	Buchnera sp. genomic DNA SEQ ID NO:1.	
XX	Buchnera; cockroach-symbiotic bacterium; cockroach extermination;	
KW	circular; ds.	

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XX 07-APR-2000; 2000JP-0107160.
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX WPI; 2002-126043/17.
XX A genomic DNA of cockroach-symbiotic bacterium
XX Claim 1; Page 16-230; 237pp; Japanese.
XX The present invention describes a gene (I) derived from Buchnera sp.
XX containing the DNA (a) or (b), (a) has a fully defined base pair
XX sequence selected from a table of sequences found in the Buchnera sp.
XX genomic DNA of ABA92787 given in the specification or is a DNA selected
XX from complementary DNA sequences, and (b) is a DNA which hybridizes with
XX the DNA (a) and encodes a protein. Also described are: (1) a recombinant
XX vector (II) containing (I); (2) a transformant (III) containing (II);
XX (3) a genomic DNA of Buchnera sp. containing the sequence given in
XX ABA92787; (4) a plasmid derived from Buchnera sp. containing DNA (c) or
XX or ABB92789 and (d) is a plasmid which hybridizes with a DNA; and (5) a
XX method for the preparation of a protein in which (III) is cultured and
XX the expression protein of the object of the present invention is collected from the
XX resultant culture. The DNA is useful for developing agricultural
XX chemicals for exterminating cockroaches. The present sequence represents
XX the specifically claimed Buchnera sp. genomic DNA sequence, from the
XX present invention.
XX Sequence 640681 BP; 237522 A; 83822 C; 84757 G; 234580 T; 0 other;
XX
XX Query Match 21.5%; Score 108.6; DB 24; Length 640681;
XX Best Local Similarity 79.6%; Pred. No. 2.9e-25;
XX Matches 144; Conservative 0; Mismatches 29; Indels 8; Gaps 1;
XX
XX QY 80 AGAGTACGATGGTGTAGCTAGCTGTTAGTACGCGACCCCTCATAGGTGAGGT 139
XX DB 275628 AAAAAATTGAGGCTGTAGCTAGCTAGTGTAGGCGACCCCTCATAGGTGAGGT 275687
XX
XX QY 140 CGGCAGTTCGAATCTGCCAGACCCCAACCAATCGAA-----GGGCGCATAGCTCAGCT 191
XX DB 275688 CGGTGTTCAATTCCTACTCAGGCTTACCAATAAAAAATCATCTGGGCTATAGCTCAGCT 275747
XX
XX QY 192 GGGAGAGCGCTCTTTCAGCAGGAGGTTCGATCCGCTTGGCTCCACCAT 251
XX DB 275748 GGGAGAGCGCTCTTTCAGCAGGAGGTTCGATCCGCTTGGCTCCACCA 275807
XX
XX QY 252 T 252
XX DB 275808 T 275808
XX
XX RESULT 15
XX ID AAA81460 standard; DNA; 20844 BP.
XX AC AAA81460;
XX
XX 04-DEC-2000 (first entry)
XX N. meningitidis partial DNA sequence gnm_8 SEQ ID NO:8.
XX
XX Neisseria meningitidis.
XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
XX antigen; vaccine; diagnosis; infection; antibacterial; identification;
XX Meningococcus B; MenB; ds.
XX
XX Neisseria meningitidis.
XX WO200022430-A2.
XX
XX 20-APR-2000.
XX
XX 08-OCT-1999; 99WO-US23573.

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XX 09-OCT-1998; 98US-0103794.
XX 30-APR-1999; 99US-0132068.
XX (CHIR ) CHIRON CORP.
XX
XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
XX Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
XX Rappuoli R, Pizza M;
XX WPI; 2000-318079/27.
XX
XX Isolated nucleotide sequences of Neisseria meningitidis which can be
XX used in the diagnosis and treatment of N. meningitidis infection and
XX other Neisserial infections, for example, N.gonorrhoea
XX
XX Claim 7; Page 320-326; 1760pp; English.
XX
XX The present invention describes methods of obtaining immunogenic
XX proteins from Neisseria genomic sequences. AAA81453 to AAA82414
XX represent specifically claimed Neisseria meningitidis genomic DNA
XX sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
XX Neisseria DNA sequences and their corresponding proteins; AAA81254 to
XX AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
XX isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
XX AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
XX sequences, which are all used in the exemplification of the present
XX invention. The nucleic acid sequences, protein sequences, and antibodies
XX against them, can be used in the manufacture of a composition. The
XX composition can be used as a medicament (or in the manufacture of a
XX medicament) for treating, preventing or diagnosing infection due to
XX Neisserial bacteria. For example, some of the identified proteins could
XX be components of vaccines against Meningococcus B; against all serotypes;
XX and/or against all pathogenic Neisseriae. Identification of sequences
XX from the bacterium will also facilitate production of biological probes,
XX particularly organism-specific probes. Attempts to make efficacious
XX Meningococcus B vaccines have failed mainly due to antigen tolerance.
XX Multivalent vaccines have also been tried but none have successfully
XX overcome antigenic variability. The provision of further, complete
XX sequences may provide an opportunity to identify secreted or surface
XX exposed proteins that may be presumed targets for the immune system and
XX which are not antigenically variable or at least more conserved than
XX other more variable regions.
XX
XX Sequence 20844 BP; 5244 A; 5005 C; 5645 G; 4949 T; 1 other;
XX
XX Query Match 21.5%; Score 108.4; DB 21; Length 20844;
XX Best Local Similarity 83.3%; Pred. No. 5.5e-26;
XX Matches 135; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
XX
XX QY 92 GGGTCTGTAGCTCAGTGTAGAGCGCACCCCTGATAAGGTGAGTGGCAGTTCGAA 151
XX DB 20552 GGGTTTGTAGCTCAGTGTAGAGCACACGCTTGTATAGCGTGGGTGCGAGTTCAG 20611
XX
XX QY 152 TCTGCCAGACCCACCAATCGAAGGGGCCATAGCTAGCTGGGAGAGCGCTGCTTGC 211
XX DB 20612 TCCTCCAGAGCCACCAACCA-GAACGGGGCATAGCTAGTGGTAGAGCACCTGCTTGC 20670
XX
XX QY 212 GCGAGGAGGTGAGCGGTTCGATCCCGTTCGCTCCACCATTA 253
XX DB 20671 AGCAGGGGGTTCATCGGTTCGATCCCGTTCGCTCCACCATTA 20712
XX
XX Search completed: February 1, 2003, 01:37:21
XX Job time : 358.347 secs

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:17:06 ; Search time 26.2031 Seconds  
(without alignments)  
5898.736 Million cell updates/sec

Title: US-09-931-486-113  
Perfect score: 504  
Sequence: 1 ATCAGAGACACCGCTTCGT.....CAGATTCCTGGGGTTATAT 504

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 1533381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	504	100.0	504	3	US-08-765-332-113	Sequence 113, App
2	504	100.0	504	4	US-09-448-894-113	Sequence 113, App
3	265.4	52.7	499	3	US-08-765-332-114	Sequence 114, App
4	265.4	52.7	499	4	US-09-448-894-114	Sequence 114, App
5	249.4	49.4	520	3	US-08-765-332-112	Sequence 112, App
6	249.4	49.4	520	4	US-09-448-894-112	Sequence 112, App
7	225.8	44.8	471	3	US-08-765-332-111	Sequence 111, App
8	225.8	44.8	471	4	US-09-448-894-111	Sequence 111, App
9	205.2	40.7	468	3	US-08-765-332-115	Sequence 115, App
10	205.2	40.7	468	4	US-09-448-894-115	Sequence 115, App
11	117.2	23.3	664	1	US-08-412-614-89	Sequence 89, Appl
12	117.2	23.3	664	2	US-08-412-614-85	Sequence 85, Appl
13	108.6	21.5	603	1	US-08-412-614-86	Sequence 86, Appl
14	108.6	21.5	603	2	US-08-635-761-86	Sequence 86, Appl
15	108.6	21.5	603	2	US-08-635-761-85	Sequence 85, Appl
16	108.6	21.5	603	4	US-09-312-520-86	Sequence 86, Appl
17	108.6	21.5	603	4	US-09-312-520-85	Sequence 85, Appl
18	102.8	20.4	808	3	US-08-765-332-131	Sequence 131, App
19	102.8	20.4	808	4	US-09-448-894-131	Sequence 131, App
20	102.8	20.4	808	4	US-09-448-894-132	Sequence 132, App
21	102.8	20.4	809	3	US-08-765-332-154	Sequence 154, App
22	102.8	20.4	809	4	US-09-448-894-154	Sequence 154, App
23	102.8	20.4	809	4	US-09-448-894-154	Sequence 154, App
24	99.4	19.7	654	2	US-08-635-761-89	Sequence 89, Appl
25	99.4	19.7	654	4	US-09-312-520-89	Sequence 89, Appl
26	97.8	19.4	549	1	US-08-412-614-92	Sequence 92, Appl
27	97.8	19.4	549	2	US-08-635-761-92	Sequence 92, Appl

ALIGNMENTS

RESULT 1

US-08-765-332-113

Sequence 113, Application US/08765332

Patent No. 6025132

GENERAL INFORMATION:

APPLICANT: JANNES, GEERT

APPLICANT: ROSSAU, RUDI

APPLICANT: VAN HEUVESWYN, HUGO

TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION

TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A

TITLE OF INVENTION: HYBRIDIZATION ASSAY

NUMBER OF SEQUENCES: 216

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHIVE P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08765.332

APPLICATION NUMBER: US/08765.332

FILING DATE: 23-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP95/02452

FILING DATE: 23-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95870032.0

FILING DATE: 07-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94870106.5

FILING DATE: 24-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 1487-14

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4091

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:

LENGTH: 504 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

```
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-765-332-113

Query Match      100.0%; Score 504; DB 3; Length 504;
Best Local Similarity 100.0%; Pred. No. 7e-168;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACACCGCTTCGCTATAGCTCCACACGAGTTCGTTGATTCACCTTCGGAAG 60
    |||||||
Db 1 ATCGAAGACACCGCTTCGCTATAGCTCCACACGAGTTCGTTGATTCACCTTCGGAAG 60

QY 61 GCGATTGGGTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120
    |||||||
Db 61 GCGATTGGGTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120

QY 121 CCCCTGATAAGGTTGAGTTCGGCAGTTCGATCTGCCCCAGACCCACCAATCGAAGGGGCC 180
    |||||||
Db 121 CCCCTGATAAGGTTGAGTTCGGCAGTTCGATCTGCCCCAGACCCACCAATCGAAGGGGCC 180

QY 181 ATAGCTCAGCTGGGAGAGCGCTCTTTTGACGAGGAGTTCAGCGGTTGATCCCGCTT 240
    |||||||
Db 181 ATAGCTCAGCTGGGAGAGCGCTCTTTTGACGAGGAGTTCAGCGGTTGATCCCGCTT 240

QY 241 GGCTCCACCAATTAAGTCTAGTCCGCGAAGCTCAGAAATGAGTGTTCACGAGGATGAGT 300
    |||||||
Db 241 GGCTCCACCAATTAAGTCTAGTCCGCGAAGCTCAGAAATGAGTGTTCACGAGGATGAGT 300

QY 301 TGATTGCTGGGTTGACATTTGATTTCTGACTTTGCGGCGAGAACTGTTTAAAAAAT 360
    |||||||
Db 301 TGATTGCTGGGTTGACATTTGATTTCTGACTTTGCGGCGAGAACTGTTTAAAAAAT 360

QY 361 TGGGTATGTAGTAAGTAGACGATGCTGTGCTTTTACGTCGAGATGTCGCGTCAAGG 420
    |||||||
Db 361 TGGGTATGTAGTAAGTAGACGATGCTGTGCTTTTACGTCGAGATGTCGCGTCAAGG 420

QY 421 TAAATTTGCGTCTCTATGCAAAATTTTCGCGGAATGTCGCTTCAAGTTATAGACAG 480
    |||||||
Db 421 TAAATTTGCGTCTCTATGCAAAATTTTCGCGGAATGTCGCTTCAAGTTATAGACAG 480

QY 481 TAACCAAGATTGCTGGGGTTATAT 504
    |||||||
Db 481 TAACCAAGATTGCTGGGGTTATAT 504

RESULT 2
US-09-448-894-113
; Sequence 113, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; ROSSAU, RUDI
; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,894
; FILING DATE: 29-No. 6312903-1999
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; CLASSIFICATION: <Unknown>
; 07-APR-1995
; 24-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,332
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-09-448-894-113
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Query Match      100.0%; Score 504; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 7e-168;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAAGACACCGCTTCGCTATAGCTCCACACGAGTTCGTTGATTCACCTTCGGAAG 60
    |||||||
Db 1 ATCGAAGACACCGCTTCGCTATAGCTCCACACGAGTTCGTTGATTCACCTTCGGAAG 60

QY 61 GCGATTGGGTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120
    |||||||
Db 61 GCGATTGGGTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120

QY 121 CCCCTGATAAGGTTGAGTTCGGCAGTTCGAAATCTGCCAGACCCACCAATCGAAGGGGCC 180
    |||||||
Db 121 CCCCTGATAAGGTTGAGTTCGGCAGTTCGAAATCTGCCAGACCCACCAATCGAAGGGGCC 180

QY 181 ATAGCTCAGCTGGGAGAGCGCTCTTTTGACGAGGAGTTCAGCGGTTGATCCCGCTT 240
    |||||||
Db 181 ATAGCTCAGCTGGGAGAGCGCTCTTTTGACGAGGAGTTCAGCGGTTGATCCCGCTT 240

QY 241 GGCTCCACCAATTAAGTCTAGTCCGCGAAGCTCAGAAATGAGTGTTCACGAGGATGAGT 300
    |||||||
Db 241 GGCTCCACCAATTAAGTCTAGTCCGCGAAGCTCAGAAATGAGTGTTCACGAGGATGAGT 300

QY 301 TGATTGCTGGGTTGACATTTGATTTCTGACTTTGCGGCGAGAACTGTTTAAAAAAT 360
    |||||||
Db 301 TGATTGCTGGGTTGACATTTGATTTCTGACTTTGCGGCGAGAACTGTTTAAAAAAT 360

QY 361 TGGGTATGTAGTAAGTAGACGATGCTGTGCTTTTACGTCGAGATGTCGCGTCAAGG 420
    |||||||
Db 361 TGGGTATGTAGTAAGTAGACGATGCTGTGCTTTTACGTCGAGATGTCGCGTCAAGG 420

QY 421 TAAATTTGCGTCTCTATGCAAAATTTTCGCGGAATGTCGCTTCAAGTTATAGACAG 480
    |||||||
Db 421 TAAATTTGCGTCTCTATGCAAAATTTTCGCGGAATGTCGCTTCAAGTTATAGACAG 480

QY 481 TAACCAAGATTGCTGGGGTTATAT 504
    |||||||
Db 481 TAACCAAGATTGCTGGGGTTATAT 504

RESULT 3
US-08-765-332-114
; Sequence 114, Application US/08765332
```



Patent No. 6025132  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
TITLE OF INVENTION: HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-114

Query Match 52.7%; Score 265.4; DB 3; Length 499;  
Best Local Similarity 78.5%; Pred. No. 9.2e-84;  
Matches 412; Conservative 0; Mismatches 66; Indels 47; Gaps 6;

QY 1 ATCGAAGACACGGCTTCGTATAGCTCCACACGAATTCCTTATTCACATTCGCAAG 60  
DB 1 ATCGAAGACTTCAGCTTCCTTATAGTCCACACGAATTCCTTATTCACATTCGCAAA 60  
QY 61 GCGATTGGGTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
DB 61 GCGATTGGGTTAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
QY 121 CCCCTGATAAGGGTGAAGTTCGCGAGTTCGAATCTCCAGAGCCACCAATCG- 172  
DB 121 CCCCTGATAAGGGTGAAGTTCGCGAGTTCGAATCTCCAGAGCCACCAATTCGCGGATG 180  
QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTTCGTTGCACCGAGAGT 221  
DB 181 GCGAGTGAATGGGGGCATAGCTCAGCTGGGAGAGCGCTTCGTTGCACCGAGAGT 240  
QY 222 CAGCGGTTCCGCTCCGCTTGGCTCCACCATTAACCTCTAG-TCGCCGGAAGCTCAGAAATG 280

DB 241 CAGGAGTTCGATCCTCTGGCTCCACCATCAACTCAGCATCGCTGAAAGCTCAGAAATG 300  
QY 281 AGTGTTCACCGAGATGAGTTGATTCGCTGGTGGTGAACATTCATTCGACATTCGCGCC 340  
DB 301 AACATT-----GGTAGTTCAATGTTGATTCGCTGGTTCGCGCC 339  
QY 341 AGAATCTGTTCTTAAATAATTTGGGTATGTATAGAGTAGACCGGATGTTGCTTTCAC 400  
DB 340 AGAATCTGTTCTTAAATAATTTGGGTATGTATAGAGTAGACCTAACACGCG- 395  
QY 401 GCGACATGTCGCGTCAAGTAAATTTGCGTTCCTCTATGCAAAATTTTCGCGCAATGT 460  
DB 396 CTGCACGTTGTTAATCAAGGCAAAATTTGCGAGTTC-AAAGCGGAATTTTCGCGCAATGT 454  
QY 461 CGTCTTCACGTTA-TAGACAGTAACAGATTCGCTTGGGCTTATAT 504  
DB 455 CGTCTTCACGTTACGAATCTATAACCAAGATTGCTTGGGGTTATAT 499

RESULT 4  
US-09-448-894-114  
Sequence 114, Application US/09448894  
Patent No. 6312903  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-6312903-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

```
;
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-09-448-894-114

Query Match          52.7%; Score 265.4; DB 4; Length 499;
Best Local Similarity 78.5%; Pred. No. 9.2e-84;
Matches 412; Conservative 0; Mismatches 66; Indels 47; Gaps 6;

QY 1 ATCGAAGACACCGGCTTCGTATAGCTCCACACGAATTCGTTGATTCACCTTCGGAAG 60
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 ATCGAAGACTTCAGCTTCCTTCATAAGTTCACACACGAATTCGTTGATTCACCTTCGGAAG 60

QY 61 GCATTTGGTTAGACCCGAGAGTACGATTCGCTGTAGCTCAGTTGGTTAGAGCGCA 120
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 GCATTTGGTTAGACCCGAGAGTACGATTCGCTGTAGCTCAGTTGGTTAGAGCGCA 120

QY 121 CCCTGATTAAGGTGAGGTGCGGAGTTCGAATTCGCCAGACCCCAATCG----- 172
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 121 CCCTGATTAAGGTGAGGTGCGGAGTTCGAATTCGCCAGACCCCAATTCGCGGAGT 180

QY 173 -----AAGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGAGGAGT 221
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 181 GCAGGTGTCAAATGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGAGGAGT 240

QY 222 CAGCGTTTCGATCCCGCTTGGCTCCACGATTAAGTCTAG-TCCGCCAAAAGCTCAGAAATG 280
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 241 CAGGAGTTCGATCCCTTGGCTCCACCATCACTCAGCATCGCTGAAAGCTCAGAAATG 300

QY 281 AGTGTTTTACCAGGATCAGGTGATTGCCCTGGTTGAACATTTGATTTCTGGACTTTCGCGC 340
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 301 ACATTT-----GGTAGTTCATGTTGATTTCTGGTCTTTTCGCGC 339

QY 341 AGAAGTGTCTTTAAATTTGGGTATGTAGTAGAGTAGAGATGAGCGATGTTGTTTCACT 400
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 340 AGAAGTGTCTTTAAATTTGGGTATGTAGTAGAGTAGAGTGAACAGCG---TGTTCA 395

QY 401 GCAGCATGTCGCTCAAGTAAATTTGCGTGTCTCTATCAAAATTTTCGCGGAATCT 460
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 396 CTGCAAGTGTGTAATCAGGCAAAATTTGCGAGTTC-AAGCGGAAATTTTCGCGGAATCT 454

QY 461 CGTCTTACGTTA-TAGACAGTAACCAAGATTCGTTGGGTTATAT 504
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 455 CGTCTTACGTTACGAATCTATAACCAAGATTCGTTGGGTTATAT 499

RESULT 5
US-08-765-332-112
; Sequence 112, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765.332
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: WO PCT/BP95/02452
; FILING DATE: 23-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B. J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-765-332-112

Query Match          49.4%; Score 249; DB 3; Length 520;
Best Local Similarity 74.4%; Pred. No. 5.7e-78;
Matches 392; Conservative 0; Mismatches 105; Indels 30; Gaps 5;

QY 1 ATCGAAGACACCGGCTTCGTATAGCTCCACACGAATTCGTTGATTCACCTTCGGAAG 60
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Db 1 ATCGAAGACATCAGCTTCCTTCATAAGTATCCACACGAATTCGTTGATTCACCTTCGGAAG 60

QY 61 GCATTTGGTTAGACCCGAGAGTTCGAATTCGCCAGACCCCAATCG----- 120
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 ATGCTGTACGCCAGCCGCTGTTATAT-----GCTCTGTAGCTCAGTTGGTTAGAGCGCA 114

QY 121 CCCTGATTAAGGTGAGGTGCGGAGTTCGAATTCGCCAGACCCCAATCG----- 172
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 115 CCCTGATTAAGGTGAGGTGCGGAGTTCGAATTCGCCAGACCCCAATTCGCTTGGTCTG 174

QY 173 -----AAGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGAGGAGTCA 224
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 175 AGAAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTGCACGAGGAGTCA 234

QY 225 CGGTTCGATCCCGCTTGGCTCCACCATTAAGTTCGCTGTAGTTCGCTGCTTTGAGCGGTA 284
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 235 CGGTTCGATCCCGCTTGGCTCCACCATCTCTCGTGTTCGGGTGAGTGTAAAGAGTCA 294

QY 285 TTTACCAGGATGAGGTGATTGCTGCTGGGTGAACATTTCTGGACTTT-----GCG 338
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 295 GAAATGATCGCGCTTCAGGTTTGTCTGTTGAGTGTGCTGATTCTGGTCTTTGACCGGTA 354

QY 339 CAGAACTGTTCTTTAAAAATTTGGGTATGTAGTAGAGTAGACCATGTTGCTTTCA 398
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 355 CGAAAAATCGTTCTTTAAAAATTTGGATATGTAGTAGAAGT-GACTGATTAATTTGCTTCA 413

QY 399 CTGCGAGCATGTCGCGTCAAGGTAAAAATTTG-CGTGCTCTCTATCAAAATTTTCGCGCAA 457
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 414 CTGGCAATGATCTGCTCAAGGTAAAAATTTGTAGTCTCTCAAGACGCAAAATTTTCGCGCAA 473

QY 458 TGTCTGCTTCACGTTATAGACAGTAACCAAGATTCGTTGGGTTATAT 504
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 474 TGTCTGCTTCACGTTAGACAGTAACCAAGATTCGTTGGGTTATAT 520

RESULT 6
US-09-448-894-112
; Sequence 112, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
```

ROSSAU, RUDI  
VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY

NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-1999  
CLASSIFICATION: <Unknown>  
24-JUN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 112:  
US-09-448-894-112

Query Match 49.4%; Score 249; DB 4; Length 520;  
Best Local Similarity 74.4%; Pred. No. 5.7e-78;  
Matches 392; Conservative 0; Mismatches 105; Indels 30; Gaps 5;  
QY 1 ATCGAAGACACCGGTTCTGTCATAGCTCCACACAAATGCTTATTCACCTGCGAAAG 60  
DB 1 ATCGAAGACATCAGCTTCTTCATAGTATCCACACAAATGCTTATTCATAGTCGAAG 60  
QY 61 GCGATTGGTTAGACCCGAGAGTACGATTGGGTCTGAGTCTAGTTAGAGCGCA 120  
DB 61 AATGTGTAAACGCGACCCGTTGTTATA-----GGTCTGAGTCTAGTTGGTTAGAGCGCA 114  
QY 121 CCCCTGATAAGGTGAGGTCGCGAGTTCGAATCTGCCAGACCCACCAATCG-----172  
DB 115 CCCCTGATAAGGTGAGGTCGCGAGTTCGAATCTGCCAGACCCACCAATCGTTGGTCG 174  
QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACACGAGGTGCG 224  
DB 175 AGAAGATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACACGAGGTGCG 234  
QY 225 CGGTTGATCCCGCTGGCTCCACCATTAACCTCTAGTCCCGGAAAGCTCAGAAATGAGTG 284  
DB 235 CGGTTGATCCCGCTGGCTCCACCATTAACCTCTCTCGTGTTCGCGTGTGTTAAAGATTCA 294

QY 285 TTATACAGGATGAGGTTGATTGCTGGTTGAACATTGATTCTGGACTTT-----GCG 338  
DB 295 GAAATGATCGCGTTTCAGGTTTCTGCTGTTGAGTCTGATTCTGGTCTTTTACCGGTA 354  
QY 339 CCAGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAGTACGAGTGTGTTGCTTTCA 398  
DB 355 CGAAAAATCGTTCTTTAAAAATTTGGGTATGTGATAGAGT-GACTGATTAAATGCTTTCA 413  
QY 399 CTGGCAGCATGTCGCGTCAAGTAAATTTG-CGTGTTCTCTATGCAAAATTTTCGGCGAA 457  
DB 414 CTGGCAATTGATCTGCTCAAGTAAATTTGTAGTTCTCAAGACGCAAAATTTTCGGCGAA 473  
QY 458 TGTGCTCTTACAGTTATAGACAGTAAACGAGTGTGTTGGGTTATAT 504  
DB 474 TGTGCTCTTACAGTTATAGACAGTAAACGAGTGTGTTGGGTTATAT 520

RESULT 7  
US-08-765-332-111  
; Sequence 111, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
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; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 111:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 471 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-765-332-111



```

; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; TITLE OF INVENTION: HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,332
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/02452
; FILING DATE: 23-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-765-332-115

Query Match 40.7%; Score 205.2; DB 3; Length 468;
Best Local Similarity 74.7%; Pred. No. 1.5e-62;
Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;

Qy 1 ATCGAAGACACCGGCTTCGTCATAGCTCCACACGAAATGCTTGTGATTCACCTGCGGAAG 60
Db 1 ATCGACGACATCAGCTGTCTCATAGCTCCACACGAAATGCTTGTGATTCACCTGCGGAAG 59
Qy 61 GCGATTGGTTAGACCGGAGTAAGATTGGTGTGAGTCTAGCTCAGTTGTTAGAGGCCA 120
Db 60 ACGATTAGTTAGCAACCTT-----CGATTGGTCTGTAGCTCAGTTGTTAGAGGCCA 113
Qy 121 CCCCTGATAAGGGTGAAGTCCGCGAGTTCGAATCTGCCACGAGGTCAGCGTTCGATCCGCT 179
Db 114 CCCCTGATAAGGGTGAAGTCCGCGAGTTCGAATCTGCCACGAGGTCAGCGTTCGATCCGCT 173
Qy 180 CATAGCTCAGTGGGAGAGCCCTGCTTTCGACCGAGGTCAGCGTTCGATCCGCT 239
Db 174 CATAGCTCAGTGGGAGAGCCCTGCTTTCGACCGAGGTCAGCGTTCGATCCGCT 233
Qy 240 TGGCTCCACCATTAACCTAGTTCGCGGAAAGCTCAGAAATGAGTGTTCACGAGGATGAGG 299
Db 234 TGGCTCCACCATTAACCTAGTTCGCGGAAAGCTCAGAAATGAGTGTTCACGAGGATGAGG 274
Qy 300 TTGATTGCTGGTTGAACATGATTCTTGGACTTTGCGCAGAACTGTTCTTTAAAAAT 359
Db 300 TTGATTGCTGGTTGAACATGATTCTTGGACTTTGCGCAGAACTGTTCTTTAAAAAT 359

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Db 275 ATGAATATCCGTCGAATATTGATTTCGAACCTTT--ATCAGAATCGTTCTTTAAAAAT 332
Qy 360 TTGGGTATGTATAGAGTAGA--CCGATGTGTTCTTCTTCTACTGCGACAGATGTCGCGTCAA 418
Db 333 TTGGGTATGTATAGAGTAGA--CCGATGTGTTCTTCTTCTACTGCGACAGATGTCGCGTCAA 392
Qy 419 GGTAAATTTGCGTGTCTCTATGCAAAATTTTCGCGAAATGCTGCTTCTTCTTCTTATAGAC 478
Db 393 GGTAAATTTGCGTGTCTCTATGCAAAATTTTCGCGAAATGCTGCTTCTTCTTATAGAC 478
Qy 479 AGTAACACAGATTGCTTGGGTTATAT 504
Db 445 --TAACACAGATTGCTTGGGTTATAT 468

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RESULT 10
US-09-448-894-115
; Sequence 115, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; VAN HEUVERSWYN, HUGO
; ROSSAU, RUDI
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,894
; FILING DATE: 29-NOV-1999
; CLASSIFICATION: <Unknown>
; 07-APR-1995
; 24-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,332
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-448-894-115

Query Match 40.7%; Score 205.2; DB 4; Length 468;
Best Local Similarity 74.7%; Pred. No. 1.5e-62;

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Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;

QY 1 ATCGAAGACACGGGTTCTGTCATAGCTCCACACAGTTCCTGATTCACCTTCGCAAG 60  
Db 1 ATCGAAGACACGGGTTCTGTCATAGCTCCACACAGTTCCTGATTCACCTTCGCAAG 59

QY 61 GCGATTGGTTTAGACCCGAGAGTAACGATGGGTCTAGCTAGTGGTTAGAGCGCA 120  
Db 60 AGATTAGTTAGCAACCTT-----CGATTGGGTCTAGCTAGTGGTTAGAGCGCA 113

QY 121 CCCCTGATAAGGGTGGAGTTCGAGTTCGAATCTGCCAGACCCACCAAA-TCGAAGGGC 179  
Db 114 CCCCTGATAAGGGTGGAGTTCGAGTTCGAATCTGCCAGACCCACCAAA-TCGAAGGGC 173

QY 180 CATAGCTCAGCTGGAGAGCCCTGCTTTTGCACGAGGAGTTCAGCGTTCGATCCCGCT 239  
Db 174 CATAGCTCAGCTGGAGAGCCCTGCTTTTGCACGAGGAGTTCAGCGTTCGATCCCGCT 233

QY 240 TGGCTCCACCAATTAACCTAGTCCGCGAAGCTCAGAAATGAGTGTTCACAGGATGAGG 299  
Db 234 TGGCTCCAC-----ACCCCGCTTGCAGCTTGTGCAAGCTTAGAA 274

QY 300 TTGATGCTGGTGGTGAACATGATTTCTGGACTTTGGCCGAGAACTGTTCTTTAAATAAT 359  
Db 275 ATGAATATTCGCTGCAATATGATTTCTGAACCTT--ATCAGATCGTCTTTAAATAAT 332

QY 360 TTGGTATGTCATAGAAGTAGA--CCGATGTTGCTTTCTACTGGCAGCATGTCGCGTCAA 418  
Db 333 TTGGTATGTCATAGAAGTAGA--CCGATGTTGCTTTCTACTGGTGTGTTGTTAGGCTAA 392

QY 419 GGTAAATTTGCGTGTCTCTATCAAAATTTTCGCGAAATGTCGCTCTCAGGTTATAGAC 478  
Db 393 GGTAAATTTGCGTGTCTCTATCAAAATTTTCGCGAAATGTCGCTCTCAGGTTATAGAC 478

QY 479 AGTAACAGATGCTTGGGGTTATAT 504  
Db 445 --TAACAGATGCTTGGGGTTATAT 468

## RESULT 11

US-08-412-614-89  
; Sequence 89, Application US/08412614  
; Patent No. 5536638  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; APPLICANT: Van Heuverswyn, Hugo  
; TITLE OF INVENTION: Hybridization Probes Derived from the  
; TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the  
; TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5536638west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402-4131  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity  
; COMPUTER: IBM PC compatible (Compaq Deskpro 286e)  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect Version #5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/412,614  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,394  
; FILING DATE: 17-DEC-1992  
; APPLICATION NUMBER: PCT/EP91/00743  
; FILING DATE: 18-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB/90901054.3

## RESULT 12

US-08-412-614-85  
; Sequence 85, Application US/08412614  
; Patent No. 5536638  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; APPLICANT: Van Heuverswyn, Hugo  
; TITLE OF INVENTION: Hybridization Probes Derived from the  
; TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the  
; TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5536638west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402-4131  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity  
; COMPUTER: IBM PC compatible (Compaq Deskpro 286e)  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect Version #5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/412,614  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,394  
; FILING DATE: 17-DEC-1992  
; APPLICATION NUMBER: PCT/EP91/00743  
; FILING DATE: 18-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB/90901054.3

; FILING DATE: 18-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A.  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.75-USWO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 89:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 664 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Neisseria meningitidis  
; STRAIN: NCTC 10025  
; US-08-412-614-89

Query Match 23.3%; Score 117.2; DB 1; Length 664;  
Best Local Similarity 82.7%; Pred. No. 1.9e-31;  
Matches 134; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGTCGAGGTCGCGAGTTCCAA 151  
Db 100 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGTCGAGGTCGCGAGTTCCAA 159

QY 152 TCTGCCAGACCCACCAATCGAAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTTGA 211  
Db 160 TCTGCCAGACCCACCAATCGAAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTTGA 219

QY 212 CGCAGGAGGTCAGCGGTCGATCCCGCTTGGCTCCACCAATA 253  
Db 220 AGCAGGGGTCATCGGTTTCGATCCCGCTTGGCTCCACCAATA 261

FILING DATE: 18-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75-USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Neisseria gonorrhoeae  
STRAIN: NCTC 8375  
US-08-412-614-85

Query Match 21.5%; Score 108.6; DB 1; Length 603;  
Best Local Similarity 84.3%; Pred. No. 2e-28;  
Matches 134; Conservative 0; Mismatches 24; Indels 1; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGGCAGTTTCGAA 151  
DB 99 GGGTTTGTAGCTCAGCTGGTTAGAGCACACCGCTTGATAGCGTGGAGTGGAGGTTCAAG 158  
QY 152 TCTGCCACAGACACCAATCAAGAGGCGCATAGCTCAGTGGAGAGCGCCTGCTTTGCA 211  
DB 159 TCTCCACAGACCAACCAA-GAAGCGGGGCGCATAGCTCAGTTGGTGGAGACCTCTTTGCA 217  
QY 212 CGCAGGAGGTGAGGTTGATCCCGCTTGGCTCCACCA 250  
DB 218 AGCAGGGGTCATCGGTTGATCCCGCTTGGCTCCACCA 256

RESULT 13  
US-08-412-614-86  
Sequence 86, Application US/08412614  
Patent No. 5536638  
GENERAL INFORMATION:  
APPLICANT: Rossau, Rudi  
APPLICANT: Van Heuverswyn, Hugo  
TITLE OF INVENTION: Hybridization Probes Derived from the  
TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the  
TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 No. 5536638west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402-4131  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity  
COMPUTER: IBM PC compatible (Compaq Deskpro 286e)  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/412,614  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,394  
FILING DATE: 17-DEC-1992  
APPLICATION NUMBER: PCT/EP91/00743  
FILING DATE: 18-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB/90901054.3

FILING DATE: 18-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75-USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Neisseria gonorrhoeae  
STRAIN: ITM 4367  
US-08-412-614-86

Query Match 21.5%; Score 108.6; DB 1; Length 603;  
Best Local Similarity 84.3%; Pred. No. 2e-28;  
Matches 134; Conservative 0; Mismatches 24; Indels 1; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGGCAGTTTCGAA 151  
DB 99 GGGTTTGTAGCTCAGCTGGTTAGAGCACACCGCTTGATAGCGTGGAGTGGAGGTTCAAG 158  
QY 152 TCTGCCACAGACCAATCAAGAGGCGCATAGCTCAGTGGAGAGCGCCTGCTTTGCA 211  
DB 159 TCTCCACAGACCAACCAA-GAAGCGGGGCGCATAGCTCAGTTGGTGGAGACCTCTTTGCA 217  
QY 212 CGCAGGAGGTGAGGTTGATCCCGCTTGGCTCCACCA 250  
DB 218 AGCAGGGGTCATCGGTTGATCCCGCTTGGCTCCACCA 256

RESULT 14  
US-08-635-761-85  
Sequence 85, Application US/08635761  
Patent No. 5945282  
GENERAL INFORMATION:  
APPLICANT: Rossau, Rudi  
TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
STREET: 3100 No. 5945282west Center, 90 S. 7th Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: U.S.A.  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: PastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/635,761  
FILING DATE: 19-APR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,394  
FILING DATE: 17-DEC-1992  
APPLICATION NUMBER: 08/412,614  
FILING DATE: 29-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75USC1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/332-5300  
TELEFAX: 612/332/9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-635-761-85

Query Match 21.5%; Score 108.6; DB 2; Length 603;  
Best Local Similarity 84.3%; Pred. No. 2e-28;  
Matches 134; Conservative 0; Mismatches 24; Indels 1; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTGGTTAGAGCGCCACCCCTGATAAGGTCGAGTCGGCAGTTTCGAA 151  
|||||  
Db 99 GGGTTGTAGCTCAGCTGGTTAGAGCACACCGCTTGATAAGCGTCGAGTCGGAGGTTCAAG 158  
||  
QY 152 TCTGCCAGAGCCACCAATCGAAGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCA 211  
|||||  
Db 159 TCCTCCAGAGCCACCAAA-GAACGGGGGCATAGCTCAGTTGGTAGAGCACCTGCTTTGCA 217  
||  
QY 212 CGCAGGAGGTGAGCGGTTGATCCCGTTGGCTCCACCA 250  
|||||  
Db 218 AGCAGGGGTCATCGGTTTCGATCCCGTTGCTCCACCA 256

## RESULT 15

US-08-635-761-86  
Sequence 86, Application US/08635761  
Patent No. 5945282  
GENERAL INFORMATION:  
APPLICANT: Rossau, Rudi  
TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
STREET: 3100 No. 5945282west Center, 90 S. 7th Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: U.S.A.  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/635,761  
FILING DATE: 19-APR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,394  
FILING DATE: 17-DEC-1992  
APPLICATION NUMBER: 08/412,614  
FILING DATE: 29-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75USC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/332-5300  
TELEFAX: 612/332/9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-635-761-86

Query Match 21.5%; Score 108.6; DB 2; Length 603;  
Best Local Similarity 84.3%; Pred. No. 2e-28;  
Matches 134; Conservative 0; Mismatches 24; Indels 1; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTGGTTAGAGCGCCACCCCTGATAAGGTCGAGTCGGCAGTTTCGAA 151  
|||||  
Db 99 GGGTTGTAGCTCAGCTGGTTAGAGCACACCGCTTGATAAGCGTCGAGTCGGAGGTTCAAG 158  
||  
QY 152 TCTGCCAGAGCCACCAATCGAAGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCA 211  
|||||  
Db 159 TCCTCCAGAGCCACCAAA-GAACGGGGGCATAGCTCAGTTGGTAGAGCACCTGCTTTGCA 217  
||  
QY 212 CGCAGGAGGTGAGCGGTTGATCCCGTTGGCTCCACCA 250  
|||||  
Db 218 AGCAGGGGTCATCGGTTTCGATCCCGTTGCTCCACCA 256

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Job time : 28.2031 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 03:05:22 ; Search time 28.0455 Seconds  
(without alignments)  
8073.649 Million cell updates/sec

Title: US-09-931-486-113  
Perfect score: 504  
Sequence: 1 ATCGAAGACACCGCTTCGT.....CAGATTGCTGGGGTTATAT 504

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues 793544  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:  
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2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	108.6	21.5	603	10	US-09-863-086-85 Sequence 85, Appl
2	108.6	21.5	603	10	US-09-863-086-86 Sequence 86, Appl
3	108.6	21.5	640681	10	US-09-790-988-1 Sequence 1, Appl
4	99.4	19.7	654	10	US-09-863-086-89 Sequence 89, Appl
5	97.8	19.4	549	10	US-09-863-086-92 Sequence 92, Appl
6	97.8	19.2	498	10	US-09-863-086-90 Sequence 90, Appl
7	95	18.8	3309400	9	US-09-738-626-1 Sequence 1, Appl
8	91.8	18.2	243	10	US-09-815-242-1358 Sequence 1358, Ap
9	91.2	18.1	255	10	US-09-815-242-1377 Sequence 1377, Ap
10	91.2	18.1	255	10	US-09-815-242-1402 Sequence 1402, Ap
11	91.2	18.1	255	10	US-09-815-242-1415 Sequence 1415, Ap
12	91.2	18.1	255	10	US-09-815-242-1423 Sequence 1423, Ap
13	91.2	18.1	255	10	US-09-815-242-1431 Sequence 1431, Ap
14	91.2	18.1	255	10	US-09-815-242-1454 Sequence 1454, Ap
15	91.2	18.1	255	10	US-09-815-242-1459 Sequence 1459, Ap
16	91.2	18.1	255	10	US-09-815-242-1473 Sequence 1473, Ap
17	91.2	18.1	255	10	US-09-815-242-1475 Sequence 1475, Ap
18	91.2	18.1	255	10	US-09-815-242-1544 Sequence 1544, Ap
19	91.2	18.1	255	10	US-09-815-242-1638 Sequence 1638, Ap

Sequence 87, Appl  
Sequence 88, Appl  
Sequence 550, App  
Sequence 4692, Ap  
Sequence 2687, Ap  
Sequence 2691, Ap  
Sequence 4361, Ap  
Sequence 4403, Ap  
Sequence 4409, Ap  
Sequence 4418, Ap  
Sequence 4386, Ap  
Sequence 8438, Ap  
Sequence 8444, Ap  
Sequence 8453, Ap  
Sequence 869, App  
Sequence 4363, Ap  
Sequence 8398, Ap  
Sequence 95, Appl  
Sequence 96, Appl  
Sequence 102, App  
Sequence 5, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 9, Appl  
Sequence 3, Appl  
Sequence 4, Appl

88.6 17.6 582 10 US-09-863-086-87  
88.6 17.6 590 10 US-09-863-086-88  
79 15.7 9797 10 US-09-070-927A-550  
76.4 15.2 290 10 US-09-815-242-4692  
76.4 15.2 495 10 US-09-815-242-2687  
76.4 15.2 495 10 US-09-815-242-2691  
72.8 14.4 76 10 US-09-974-300-4361  
72.8 14.4 76 10 US-09-974-300-4403  
72.8 14.4 76 10 US-09-974-300-4409  
72.8 14.4 76 10 US-09-974-300-4418  
72.8 14.4 76 10 US-09-974-300-8396  
72.8 14.4 76 10 US-09-974-300-8438  
72.8 14.4 76 10 US-09-974-300-8444  
72.8 14.4 76 10 US-09-974-300-8453  
72.2 14.3 1069 10 US-09-070-927A-869  
70.8 14.0 74 10 US-09-974-300-4363  
70.8 14.0 76 10 US-09-974-300-8398  
69.8 13.8 246 10 US-09-863-086-95  
69.8 13.8 279 10 US-09-863-086-96  
69.8 13.8 2336 10 US-09-842-552-102  
68.6 13.6 836 9 US-09-894-467-5  
65 12.9 1919 10 US-09-927-483-1  
65 12.9 1919 10 US-09-927-483-2  
64.8 12.9 108 12 US-10-046-722-9  
63 12.5 1883 10 US-09-927-483-3  
63 12.5 1883 10 US-09-927-483-4

## ALIGNMENTS

## RESULT 1

US-09-863-086-85  
; Sequence 85, Application US/09863086  
; Patent No. US20020048762A1

## GENERAL INFORMATION:

APPLICANT: Rossau, Rudi  
TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
REGION BETWEEN THE 16S A

## NUMBER OF SEQUENCES: 104

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant, Gould, Smith, Edell, Weiler & Schmidt  
STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street  
CITY: Minneapolis  
STATE: MN

COUNTRY: U.S.A.  
ZIP: 55402

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/863,086

FILING DATE: 22-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/312,520

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/412,614

FILING DATE: 29-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hillson, Randall A

REGISTRATION NUMBER: 31,838

REFERENCE/DOCKET NUMBER: 8076.75USC1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/332-5300

TELEFAX: 612/332/9081

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

LENGTH: 603 base pairs

TYPE: nucleic acid

```
;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-09-863-086-85

Query Match          21.5%; Score 108.6; DB 10; Length 603;
Best Local Similarity 84.3%; Pred. No. 1.4e-26;
Matches 134; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

QY 92 GGGTCTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAAGGGTGGAGGTCGGCAGTTCGAA 151
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 GGGTTTGTAGCTCAGCTGAGTTAGAGCACACGCTTGATAGCGTGAGGTCGGAGGTTCAAG 158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 152 TCTGCCAGACCCACCAATCGAAGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCA 211
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 TCTCCAGACCCACCAAA-GAAGCGGGGCATAGCTCAGTTGGTAGAGCACCTGCTTTGCA 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 212 CGCAGGAGGTCAGCGGTTCCGCTCCGCTTGCTCCACCA 250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 AGCAGGGGGTCATCGGTTCCGCTCCGCTTGCTCCACCA 256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 2
US-09-863-086-86
; Sequence 86, Application US/09863086
; Patent No. US20020048762A1
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER
; REGION BETWEEN THE 16S A
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. US20020048762Alwest Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,086
; FILING DATE: 22-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/312,520
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/412,614
; FILING DATE: 29-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hillson, Randall A
; REGISTRATION NUMBER: 31,838
; REFERENCE/DOCKET NUMBER: 8076.75USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332/9081
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
```

```
;
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-863-086-86

Query Match          21.5%; Score 108.6; DB 10; Length 603;
Best Local Similarity 84.3%; Pred. No. 1.4e-26;
Matches 134; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

QY 92 GGGTCTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAAGGGTGGAGGTCGGCAGTTCGAA 151
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 GGGTTTGTAGCTCAGCTGAGTTAGAGCACACGCTTGATAGCGTGAGGTCGGAGGTTCAAG 158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 152 TCTGCCAGACCCACCAATCGAAGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTGCA 211
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 TCTCCAGACCCACCAAA-GAAGCGGGGCATAGCTCAGTTGGTAGAGCACCTGCTTTGCA 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 212 CGCAGGAGGTCAGCGGTTCCGCTCCGCTTGCTCCACCA 250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 AGCAGGGGGTCATCGGTTCCGCTCCGCTTGCTCCACCA 256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, YOSAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
; US-09-790-988-1

Query Match          21.5%; Score 108.6; DB 10; Length 640681;
Best Local Similarity 79.6%; Pred. No. 5.5e-25;
Matches 144; Conservative 0; Mismatches 29; Indels 8; Gaps 1;

QY 80 AGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAAGGGTGAAGT 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275628 AAAAAAATTAGAAGGCTTGTAGCTCAGATGTTAGAGCGCACCCCTGTGATAAGGGTGAAGT 275687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 140 CGGCAGTTTGAATCTGCCAGAGACCCACCAATCGAA-----GGGGCCATAGCTCAGCT 191
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275688 CGGTGGTTCAATTCCACTCAGGCGCTACCAATAAAAAATATCTGGGGCTATAGCTCAGCT 275747
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 192 GGGAGAGCGCTGCTTTTGGACGAGGAGGTCAGCGGTTCCGCTCCGCTTGCTCCACCAT 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275748 GGGAGAGCGCTGCTTGCACGCGAGGAGGTCAGCGGTTCCGCTCCGCTTGCTCCACCAT 275807
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 252 T 252
Db 275808 T 275808

RESULT 4
US-09-863-086-89
; Sequence 89, Application US/09863086
; Patent No. US20020048762A1
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudi
```

;; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
;; REGION BETWEEN THE 16S A

;; NUMBER OF SEQUENCES: 104

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
;; STREET: 3100 No. US20020048762Alwest Center, 90 S. 7th Street

;; CITY: Minneapolis

;; STATE: MN

;; COUNTRY: U.S.A.

;; ZIP: 55402

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSeq Version 1.5

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/863,086

;; FILING DATE: 22-May-2001

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 09/312,520

;; FILING DATE: <Unknown>

;; APPLICATION NUMBER: 08/412,614

;; FILING DATE: 29-MAR-1995

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hillson, Randall A

;; REGISTRATION NUMBER: 31,838

;; REFERENCE/DOCKET NUMBER: 8076.75USC1

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 612/332-5300

;; TELEFAX: 612/332/9081

;; TELEX: <Unknown>

;; INFORMATION FOR SEQ ID NO: 89:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 654 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: Genomic DNA

;; HYPOTHETICAL: NO

;; ANTI-SENSE: NO

;; FRAGMENT TYPE: <Unknown>

;; ORIGINAL SOURCE:

;; SEQUENCE DESCRIPTION: SEQ ID NO: 89:

;; US-09-863-086-89

Query Match 19.7%; Score 99.4; DB 10; Length 654;

Best Local Similarity 81.6%; Pred. No. 1.8e-23;

Matches 115; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 113 AGACGGCACCCCTGATAAGGCTGAGGTGCGGAGTTCGATCTGCCAGACCCACCAATCG 172

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 111 AGACGACACGCTTGATAAGGCTGAGGTGCGGAGTTCGATCTGCCAGACCCACCAAGAA 170

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

QY 173 AAGGGGCGATAGCTACGCTGGGAGCGCTGCTTTTCAGCAGGAGGTGAGCGGTTGCGA 232

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 171 CGGGGGCGATAGCTACGCTGGGAGCGCTGCTTTTCAGCAGGAGGTGAGCGGTTGCGA 230

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

QY 233 TCCCGCTTGGCTCCACCAATTA 253

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 231 TCCCGCTTGGCTCCACCAATTA 251

RESULT 5

US-09-863-086-92

; Sequence 92, Application US/09863086

; Patent No. US20020048762A1

; GENERAL INFORMATION:

; APPLICANT: Rossau, Rudi

; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER

; REGION BETWEEN THE 16S A

; NUMBER OF SEQUENCES: 104

; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
;; STREET: 3100 No. US20020048762Alwest Center, 90 S. 7th Street

;; CITY: Minneapolis

;; STATE: MN

;; COUNTRY: U.S.A.

;; ZIP: 55402

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSeq Version 1.5

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/863,086

;; FILING DATE: 22-May-2001

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 09/312,520

;; FILING DATE: <Unknown>

;; APPLICATION NUMBER: 08/412,614

;; FILING DATE: 29-MAR-1995

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hillson, Randall A

;; REGISTRATION NUMBER: 31,838

;; REFERENCE/DOCKET NUMBER: 8076.75USC1

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 612/332-5300

;; TELEFAX: 612/332/9081

;; TELEX: <Unknown>

;; INFORMATION FOR SEQ ID NO: 92:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 549 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: Genomic DNA

;; HYPOTHETICAL: NO

;; ANTI-SENSE: NO

;; FRAGMENT TYPE: <Unknown>

;; ORIGINAL SOURCE:

;; SEQUENCE DESCRIPTION: SEQ ID NO: 92:

;; US-09-863-086-92

Query Match

Best Local Similarity 19.4%; Score 97.8; DB 10; Length 549;

Matches 132; Conservative 0; Mismatches 37; Indels 2; Gaps 1;

QY 89 ATTGGTCTGTAGCTAGCTAGTGTGTTAGAGCGCACCCCTGATAAGGGTGTAGGTGCGGAGTTC 148

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 59 ATTGGTCTGTAGCTAGCTAGTGTGTTAGAGCGCACCCCTGATAAGGGTGTAGGTGCGGAGTTC 118

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

QY 149 GAATCTGCCAGACCCACCAATCGAAGGGCCATAGCTAGCTAGGAGCGCCCTGCTTT 208

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 119 AAGTCTTATAGTACCCACCAATT--TTGGGGTTATAGCTAGTGTGTTAGAGCGCCCTGCTTT 176

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

QY 209 GCACGCGAGGAGTTCAGCGGTTGCGATCCCTTGGTCCACCAATTAACTCTA 259

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

Db 177 GCACGCGAGGAGTTCAGCGGTTGCGATCCCTTGGTCCACCAATTAACTCTA 227

||||| ||| ||||||| ||| ||||||| ||| ||| ||||||| |||||||

RESULT 6

US-09-863-086-90

; Sequence 90, Application US/09863086

; Patent No. US20020048762A1

; GENERAL INFORMATION:

; APPLICANT: Rossau, Rudi

; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER

; REGION BETWEEN THE 16S A

; NUMBER OF SEQUENCES: 104

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt

; STREET: 3100 No. US20020048762Alwest Center, 90 S. 7th Street

; CITY: Minneapolis

; STATE: MN





```
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1415
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1415

Query Match      18.1%; Score 91.2; DB 10; Length 255;
Best Local Similarity 78.4%; Pred. No. 6.1e-21;
Matches 127; Conservative 0; Mismatches 23; Indels 12; Gaps 1;

QY 85 AACGATTGGCTCTAGTCAGTGGTGTAGAGCGCACCCCTGATAGGGTGAAGGTCAGGTCGGCA 144
   || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 162 AATTAATGGCCCTATAGTCAGTCAGTGGTGTAGAGCGCACCCCTGATAGGGTGAAGGTCGGTG 103
   ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 145 GTTCGAATCTGCCAGACCCACCA-----ATCGAAGGGGCCATAGCTCAGCTG 192
   ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 102 GTTCGAGTCCACTTAGGCCACCACTTAATTAATACCTATTTGGGGCTTAGCTCAGCTG 43
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 193 GGAGAGCGCTGCTTTGCAGCGCAGGAGGTGACGGTTTCGATC 234
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 42 GGAGAGCGCTGCTTTGCAGCGCAGGAGGTGACGGTTTCGATC 1

RESULT 12
US-09-815-242-1423/c
; Sequence 1423, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1431
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1431
```

```
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1415
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-1415

Query Match      18.1%; Score 91.2; DB 10; Length 255;
Best Local Similarity 78.4%; Pred. No. 6.1e-21;
Matches 127; Conservative 0; Mismatches 23; Indels 12; Gaps 1;

QY 85 AACGATTGGCTCTAGTCAGTGGTGTAGAGCGCACCCCTGATAGGGTGAAGGTCAGGTCGGCA 144
   || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 162 AATTAATGGCCCTATAGTCAGTCAGTGGTGTAGAGCGCACCCCTGATAGGGTGAAGGTCGGTG 103
   ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 145 GTTCGAATCTGCCAGACCCACCA-----ATCGAAGGGGCCATAGCTCAGCTG 192
   ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 102 GTTCGAGTCCACTTAGGCCACCACTTAATTAATACCTATTTGGGGCTTAGCTCAGCTG 43
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 193 GGAGAGCGCTGCTTTGCAGCGCAGGAGGTGACGGTTTCGATC 234
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 42 GGAGAGCGCTGCTTTGCAGCGCAGGAGGTGACGGTTTCGATC 1

RESULT 12
US-09-815-242-1423/c
; Sequence 1423, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
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RESULT 15
US-09-815-242-1459/c
; Sequence 1459, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: zyskind, Judith W.
; APPLICANT: Walli, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in

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/ CURRENT APPLICATION NUMBER: US/09/815,242
/
/ CURRENT FILING DATE: 2001-03-21
/
/ PRIOR APPLICATION NUMBER: 60/191,078
/
/ PRIOR FILING DATE: 2000-03-21
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/ PRIOR APPLICATION NUMBER: 60/206,848
/
/ PRIOR FILING DATE: 2000-05-23
/
/ PRIOR APPLICATION NUMBER: 60/207,727
/
/ PRIOR FILING DATE: 2000-05-26
/
/ PRIOR APPLICATION NUMBER: 60/242,578
/
/ PRIOR FILING DATE: 2000-10-23
/
/ PRIOR APPLICATION NUMBER: 60/253,625
/
/ PRIOR FILING DATE: 2000-11-27
/
/ PRIOR APPLICATION NUMBER: 60/257,931
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Job time : 766.045 secs
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Search completed: February 1, 2003, 07:03:32  
Job time : 766.045 secs





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:09:56 ; Search time 940.445 Seconds  
(without alignments)  
8679.427 Million cell updates/sec

Title: US-09-931-486-113  
Perfect score: 504  
Sequence: 1 ATCGAGACACGGCTTCGT.....CAGATTGCTGGGGTTATAT 504

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em\_estba.\*  
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19: em\_gss\_inv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rtd.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	251.8	50.0	507	17	BH200120	BH200120 Sml-57J2.
C 2	248.6	49.3	629	17	BH201541	BH201541 Sml-57P13
C 3	204	40.5	639	17	AQ509640	AQ509640 nbxb0096P
4	102.6	20.4	319	10	BE092111	BE092111 IL2-BT073
5	87	17.3	497	13	BI544108	BI544108 S071 Grac
6	87	17.3	548	13	BI544155	BI544155 S129 Grac

7	85.4	16.9	539	13	BI544086	BI544086 S042 Grac
C 8	79.8	15.8	593	17	BH400944	BH400944 AG-ND-158
C 9	79.8	15.8	760	17	BH393190	BH393190 AG-ND-168
10	69.8	13.8	649	17	BH771024	BH771024 LLMGtag74
11	66.2	13.1	577	17	BH819575	BH819575 BACPP13-E
C 12	64.8	12.9	191	17	AZ578476	AZ578476 23h03 Sho
C 13	64.4	12.8	608	17	BH375641	BH375641 AG-ND-133
C 14	63	12.5	904	17	BH159957	BH159957 ENTST113TF
C 15	62.6	12.4	696	17	BH383241	BH383241 AG-ND-137
C 16	62.6	12.4	754	17	BH405252	BH405252 AG-ND-127
17	61	12.1	3268	17	BH770998	BH770998 LLMGtag72
C 18	60.2	11.9	712	17	BH397037	BH397037 AG-ND-137
C 19	57.8	11.5	287	17	BH614410	BH614410 1C22AG2 S
C 20	56.6	11.2	579	17	BH375975	BH375975 AG-ND-133
C 21	56.2	11.2	541	17	BH387664	BH387664 AG-ND-157
C 22	56	11.1	713	13	BJ096963	BJ096963 B3096963
C 23	54.8	10.9	619	9	AA680996	AA680996 SW3D9CA51
C 24	54.8	10.9	774	12	BG354849	BG354849 MBT5MLA09
C 25	54	10.7	2149	17	AQ012191	AQ012191 430P1A043
C 26	52.8	10.5	617	9	AI526132	AI526132 pc3-2.B11
27	51.8	10.3	551	10	BE092053	BE092053 IL2-BT073
28	51	10.1	679	13	BI263958	BI263958 NF107H06P
C 29	49.2	9.8	690	17	C119B2	AJ226701 Ciona int
C 30	48.2	9.6	963	17	AZ549906	AZ549906 ENTDM46TR
C 31	48	9.5	902	17	CNS06M5P	AL405059 T7 end of
32	47.6	9.4	615	17	CI6G5	AJ227395 Ciona int
C 33	47.6	9.4	938	17	AZ683938	AZ683938 ENT1J28TR
C 34	47.4	9.4	330	14	BQ205940	BQ205940 UI-R-EP0-
C 35	47	9.3	432	13	BI941477	BI941477 q079a1.Y
C 36	46.6	9.2	501	13	BJ313245	BJ313245 BJ313245
C 37	46.6	9.2	973	17	AZ688146	AZ688146 ENTLA19TR
C 38	46.4	9.2	372	10	BE092243	BE092243 IL2-BT073
C 39	46.4	9.2	901	17	AZ531501	AZ531501 ENTIC155TF
C 40	46.4	9.2	923	17	AZ540828	AZ540828 ENTDM42TF
C 41	46.2	9.2	238	10	BE491959	BE491959 EST18-2F
42	46	9.1	612	17	AQ989869	AQ989869 RfC00532
43	46	9.1	653	13	BJ318992	BJ318992 BJ318992
44	45.8	9.1	1258	17	BH770957	BH770957 LLMGtag68
C 45	45.6	9.0	905	17	AZ672622	AZ672622 ENTMR14TR

#### ALIGNMENTS

RESULT 1  
BH200120/c  
LOCUS Sml-57J2.TF Sml Schistosoma mansoni genomic clone Sml-57J2, DNA  
DEFINITION Sml-57J2.TF Sml Schistosoma mansoni genomic clone Sml-57J2, DNA  
ACCESSION BH200120  
VERSION BH200120.1 GI:16370164  
KEYWORDS GSS.  
SOURCE Schistosoma mansoni.  
ORGANISM Schistosoma mansoni  
REFERENCE 1 (bases 1 to 507)  
AUTHORS Shetty,J., Simpson,A., Malek,J., Koo,H., Loverde,P.T. and El-Sayed ,N.M.  
TITLE Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sml BAC library for gene discovery and map construction  
JOURNAL Unpublished (2001)  
COMMENT Other GSSs: Sml-57J2.TR  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
lo.edu).  
Seq primer: M13 For  
Class: BAC ends.

```

FEATURES                                     Location/Qualifiers
Source                                     1..507
/organism="Schistosoma mansoni"
/strain="Puerto Rico"
/db_xref="taxon:6183"
/clone="Sml-57J2"
/clone_lib="Sml"
/note="Vector: pBelOBAC11; Site_1: Hin dIII; Constructed
in the laboratory of Dr. Denis Le Paslier at the Fondation
Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma
mansoni agarose embedded DNA was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBelOBAC11 digested with Hin dIII. The average insert size
is 100 kb. Total clone coverage: approx. 7.95 x the
haploid genome. Further information can be found in Le
Paslier et al. (2000) Construction and characterization of
a Schistosoma mansoni bacterial artificial chromosome
library. Genomics 65: 87-94."
BASE COUNT      136 a 129 c 117 g 125 t
ORIGIN
Query Match      50.0%; Score 251.8; DB 17; Length 507;
Best Local Similarity 78.1%; Pred. No. 2.9e-68;
Matches 385; Conservative 0; Mismatches 62; Indels 46; Gaps 5;

QY 1 ATCAAGACACCGCTTCGTCATAGCTCCACACAGCAATTCCTGATTCACCTTCGGAAG 60
Db 485 ATCAAGACCTTCAGCTTCTTCATAGTTCCACACAGCAATTCCTGATTCACCTTCGGA 426
QY 61 GCGATTGGGTTTACACCCGAGAGTAAGCATTTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120
Db 425 GCGATTGGGTTGACACCCGAGAGTGACGATTTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 366
QY 121 CCCTGTATAGGGTGGAGTGGCGAGTTGGAATCTGCCAGACCCACCAATCG----- 172
Db 365 CCCTGTATAGGGTGGAGTGGCGAGTTGGAATCTGCCAGACCCACCAATTCGCGGATG 306
QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGCGAGGAGT 221
Db 305 GCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGCGAGGAGT 246
QY 222 CAGCGGTTTCGATCCGCTTGGCTCCACCAATTAACCTCTAG-TCGCCGAAAGCTCAGAATG 280
Db 245 CAGGAGTTTCGATCCCTCTGGCTCCACCAATTAACCTCTAG-TCGCCGAAAGCTCAGAATG 186
QY 281 AGTGTATTACAGGATGAGTTGATTCGCTGGGTGGAACATTTGTTTGGACTTTCGCGC 340
Db 185 AACATT-----GGTAGTTCAATGTTGATTTCTGCTTTGCGC 147
QY 341 AGAAGTGTCTTTAAATAATTTGGTATGTAGTAAGACTAGCGATGTTGCTTTTCACT 400
Db 146 AGAAGTGTCTTTAAATAATTTGGTATGTAGTAAGACTAGCGATGTTGCTTTTCACT 91
QY 401 GGCAGCATGTCGGCTCAAGTAAATTTGGCTGTTCTCTATGCAAAATTTTCGGCGAATGT 460
Db 90 CTGCAGTGTCTTAATCAAGCAAAATTTGGGAGTTC-AAGCGGGAATTTTCGGCGAATGT 32
QY 461 CGTCTTCAGTTA 473
Db 31 CGTCTTCAGTTA 19

RESULT 2
LOCUS BH201541/c 629 bp DNA linear GSS 24-OCT-2001
DEFINITION Sml-57P13.TF Sml Schistosoma mansoni genomic clone Sml-57P13, DNA
sequence.
ACCESSION BH201541
VERSION BH201541.1 GI:16373041
KEYWORDS GSS:
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

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REFERENCE
AUTHORS Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed
,N.M.
TITLE Use of end sequences from Schistosoma mansoni (Puerto Rico strain)
JOURNAL Sml BAC library for gene discovery and map construction
COMMENT Other.GSSs: Sml-57P13.TF
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org
lo.edu).
Seq primer: M13 For
Class: BAC ends.
FEATURES                                     Location/Qualifiers
Source                                     1..629
/organism="Schistosoma mansoni"
/strain="Puerto Rico"
/db_xref="taxon:6183"
/clone="Sml-57P13"
/clone_lib="Sml"
/note="Vector: pBelOBAC11; Site_1: Hin dIII; Constructed
in the laboratory of Dr. Denis Le Paslier at the Fondation
Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma
mansoni agarose embedded DNA was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBelOBAC11 digested with Hin dIII. The average insert size
is 100 kb. Total clone coverage: approx. 7.95 x the
haploid genome. Further information can be found in Le
Paslier et al. (2000) Construction and characterization of
a Schistosoma mansoni bacterial artificial chromosome
library. Genomics 65: 87-94."
BASE COUNT      157 a 172 c 146 g 154 t
ORIGIN
Query Match      49.3%; Score 248.6; DB 17; Length 629;
Best Local Similarity 77.7%; Pred. No. 3.4e-67;
Matches 383; Conservative 0; Mismatches 64; Indels 46; Gaps 5;

QY 1 ATCAAGACACCGCTTCGTCATAGCTCCACACAGCAATTCCTGATTCACCTTCGGAAG 60
Db 485 ATCAAGACCTTCAGCTTCTTCATAGTTCCACACAGCAATTCCTGATTCACCTTCGGA 426
QY 61 GCGATTGGGTTTACACCCGAGAGTAAGCATTTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120
Db 425 GCGATTGGGTTGACACCCGAGAGTGACGATTTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 366
QY 121 CCCTGTATAGGGTGGAGTGGCGAGTTGGAATCTGCCAGACCCACCAATCG----- 172
Db 365 CCCTGTATAGGGTGGAGTGGCGAGTTGGAATCTGCCAGACCCACCAATTCGCGGATG 306
QY 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGCGAGGAGT 221
Db 305 GCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCGACGCGAGGAGT 246
QY 222 CAGCGGTTTCGATCCGCTTGGCTCCACCAATTAACCTCTAG-TCGCCGAAAGCTCAGAATG 280
Db 245 CAGGAGTTTCGATCCCTCTGGCTCCACCAATTAACCTCTAG-TCGCCGAAAGCTCAGAATG 186
QY 281 AGTGTATTACAGGATGAGTTGATTCGCTGGGTGGAACATTTGTTTGGACTTTCGCGC 340
Db 185 AACATT-----GGTAGTTCAATGTTGATTTCTGCTTTGCGC 147
QY 341 AGAAGTGTCTTTAAATAATTTGGTATGTAGTAAGACTAGCGATGTTGCTTTTCACT 400
Db 146 AGAAGTGTCTTTAAATAATTTGGTATGTAGTAAGACTAGCGATGTTGCTTTTCACT 91
QY 401 GGCAGCATGTCGGCTCAAGTAAATTTGGCTGTTCTCTATGCAAAATTTTCGGCGAATGT 460

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/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 73 a 62 c 91 g 93 t  
ORIGIN

Query Match 20.4%; Score 102.6; DB 10; Length 319;  
Best Local Similarity 81.1%; Pred. No. 2.5e-21;  
Matches 142; Conservative 0; Mismatches 9; Indels 24; Gaps 1;

QY 105 AGTTGGTTAGAGCGCACCCCTGATAGGGTGAGGTGCGCAGTTCGAACTGCCAGACCC 164  
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Db 1 AGTTGGTTAGAGCGCACCCCTGATAGGGTGAGGTGCGCAGTTCGAACTGCCAGACCC 60  
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QY 165 ACCATCG-----AAGGGCCCATAGCTACGCTGGGAGAGCG 200  
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Db 61 ACCATCTGTGCGGGAAGCCTGTAGAATACGGGGCCATAGCTACGCTGGGAGAGCG 120  
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QY 201 CCTGTTTTCACGAGGAGGTGAGGTTCGATCCCGCTTGCTCCACCATTAAC 255  
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Db 121 CCTGCTTTCACGAGGAGGTCAAGGTTCGATCCCGCTTGCTCCACCATTTAC 175  
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RESULT 5  
BI544108  
LOCUS  
DEFINITION S071 Gracilaria lemaneiformis gametophyte cDNA library Gracilaria lemaneiformis cDNA 5', mRNA sequence. EST 01-MAR-2002

ACCESSION BI544108  
VERSION BI544108.1 GI:190333790  
KEYWORDS EST.

SOURCE Gracilaria lemaneiformis.  
ORGANISM Gracilaria lemaneiformis.  
Eukaryota; Rhodophyta; Florideophyceae; Gracilariiales;  
Gracilariaceae; Gracilaria.

REFERENCE 1 (bases 1 to 497)  
Sun, X., Yang, G.P., Mao, Y.X. and Zhang, X.C.  
Analysis of expressed sequence tags of a marine red alga, Gracilaria lemaneiformis  
Unpublished (2001)  
Contact: Sun, X.; Zhang, X. C.  
College of Marine Life Sciences  
Ocean University of Qingdao  
Yushan Road 5, Qingdao, 266003, Shandong, China  
Tel: +86-0532-2032789  
Fax: +86-0532-2032276  
Email: xc Zhang@ouqd.edu.cn

PCR Primers  
FORWARD: 5' -CGTGTACCATGCTCTAGAGT-3'  
BACKWARD: 5' -CTGATCTAGACCTGAGGCTC-3'  
Seq primer: 5' -CGTGTACCATGCTCTAGAGT-3'  
POLYA=No.

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Location/Qualifiers  
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/db\_xref="taxon:2778"  
/clone\_lib="Gracilaria lemaneiformis gametophyte cDNA library"  
/tissue\_type="gametophyte thalli"  
/note="Vector: pMD 18-T; Site\_1: EcoR V with a T hang; Wild type Gracilaria lemaneiformis were harvested from Zhanshan Bay, Qingdao (China). After rinsed with boiled seawater, younger thalli was cut and washed every 3-4 days until 1 month. Then thalli was cultivated in Provasoli medium. Total RNA was isolated from thalli of gametophyte algae, using UNIQ-10 Trizol Total RNA Preparation Kit (Sangon Inc., Shanghai, China). The cDNA was synthesized, amplified and cloned using cDNA Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector

(Takara Biotechnology Co., Ltd., Dalian, China), respectively. 151 a 77 c 103 g 166 t

BASE COUNT 151 a 77 c 103 g 166 t  
ORIGIN

Query Match 17.3%; Score 87; DB 13; Length 497;  
Best Local Similarity 74.5%; Pred. No. 2.8e-16;  
Matches 123; Conservative 0; Mismatches 40; Indels 2; Gaps 1;

QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTGCGCAGTTTCGAA 151  
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Db 225 GGGCTATTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTGCGCAGTTTCANA 284  
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QY 152 TCTGCCCCAGACCCACCA--ATCGAAGGGGCCATAGCTACGCTGGGAGAGCGGCTGCTTTG 209  
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Db 285 TCCAGATAGCCCAATGATAAAGGGGTATAGCTACGCTGGTGGTAGAGCGCTGCTTTG 344  
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QY 210 CACGAGGAGGTGAGCGGTTCGATCCCGCTTGCTCCACCATTA 254  
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Db 345 CAAGCAGATGTACGCGGTTCAAATCCGCTTATCTCCAGTTTAA 389  
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RESULT 6  
BI544155  
LOCUS  
DEFINITION S129 Gracilaria lemaneiformis gametophyte cDNA library Gracilaria lemaneiformis cDNA 5', mRNA sequence. EST 01-MAR-2002

ACCESSION BI544155  
VERSION BI544155.1 GI:19033837  
KEYWORDS EST.

SOURCE Gracilaria lemaneiformis.  
ORGANISM Gracilaria lemaneiformis.  
Eukaryota; Rhodophyta; Florideophyceae; Gracilariiales;  
Gracilariaceae; Gracilaria.

REFERENCE 1 (bases 1 to 548)  
Sun, X., Yang, G.P., Mao, Y.X. and Zhang, X.C.  
Analysis of expressed sequence tags of a marine red alga, Gracilaria lemaneiformis  
Unpublished (2001)  
Contact: Sun, X.; Zhang, X. C.  
College of Marine Life Sciences  
Ocean University of Qingdao  
Yushan Road 5, Qingdao, 266003, Shandong, China  
Tel: +86-0532-2032789  
Fax: +86-0532-2032276  
Email: xc Zhang@ouqd.edu.cn

PCR Primers  
FORWARD: 5' -CGTGTACCATGCTCTAGAGT-3'  
BACKWARD: 5' -CTGATCTAGACCTGAGGCTC-3'  
Seq primer: 5' -CGTGTACCATGCTCTAGAGT-3'  
POLYA=Yes.

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Location/Qualifiers  
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/note="Vector: pMD 18-T; Site\_1: EcoR V with a T hang; Wild type Gracilaria lemaneiformis were harvested from Zhanshan Bay, Qingdao (China). After rinsed with boiled seawater, younger thalli was cut and washed every 3-4 days until 1 month. Then thalli was cultivated in Provasoli medium. Total RNA was isolated from thalli of gametophyte algae, using UNIQ-10 Trizol Total RNA Preparation Kit (Sangon Inc., Shanghai, China). The cDNA was synthesized, amplified and cloned using cDNA Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector (Takara Biotechnology Co., Ltd., Dalian, China), respectively."

BASE COUNT 183 a 92 c 107 g 166 t  
ORIGIN

Db	66	GGGCTATTACTCAGTTGGTTAGAGCGCACCCCTGATAGGGTGAAGTCCCTGGTTCAAA	125
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Db	126	TCCAGGATAGCCCAACCATGAATAAGGGGTATAGTCACTGGTAGAGTGTCTTTTG	185
Qy	210	CACGACGAGGTACGCGGTTTCGATCCGGCTTGGCTCCACCATTA	254
Db	186	CAAGGCAGATGTACGCGGTTCAATACCGCTTATCTCCAAGTTTAA	230

RESULT 8	593 bp	DNA	linear	GSS 11-DEC-2001
BH4 00944/c				
LOCUS	BH4 00944			
DEFINITION	AG-ND-158022.TF	ND-TAM	Anopheles gambiae	genomic clone AG-ND-158022
				, DNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

BH400944  
 BH400944.1  
 GSS.  
 African malaria mosquito.  
 Anopheles gambiae  
 Eukaryota; Amoebozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Anopheles.  
1 (bases 1 to 593)  
Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.  
Direct Submission of BAC-end sequences from Anopheles gambiae  
Unpublished (2001)  
Other\_GSSs: AG-ND-158022.TR  
Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208

Tel: 301 838 0208  
Fax: 301 838 3543  
Email: bjoftus@tigr.org

This clone is from an *A. gambiae* BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from *A. gambiae* PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.

Seq primer: M13 For  
Class: BAC ends.

Seq primer: M13 For	
Class: BAC ends.	
FEATURES	Location/Qualifiers
source	1..593
	/organism="Anopheles gambiae"
	/strain="PEST"
	/db_xref="taxon:7165"
	/clone_lib="AG-ND-158Q22"
	/clone_lib="ND-TAM"
	/note="Vector: pECBAC1; Site_1: HindIII"
BASE COUNT	119 a 157 c 118 g 199 t
ORIGIN	
Query Match	15.8%; Score 79.8; DB 17; Length 593;
Best Local Similarity	77.4%; Pred. No. 5.9e-14;
Matches 123:	Conservative 0; Mismatches 32; Indels 4; Gaps 2

QY 158 CAGACCCACCAATCG---AAGGGGCCATAGCTCAGCTGG-GAGAGCGCCTGCTTTGCACG 213  
Db 514 CGAGACTACTAATTGAAAAGGGGAATTAGCTCAGCTGGCTAGAGCGCCTGCCTTGCACG 455  
QY 214 CAGGAGGTCAGGGTTTCGATCCCGCTTGGCTCCACCAAT 252

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Db 454 CAGGAGTCAAGGGTTCGACTCCCTTATTCTCCACAGTT 416

RESULT 9
BH393190/c
LOCUS
DEFINITION AG-ND-168H12.TR ND-TAM Anopheles gambiae genomic clone AG-ND-168H12
, DNA sequence.
ACCESSION BH393190
VERSION BH393190.1 GI:17339331
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 760)
AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: AG-ND-168H12.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
Seq primer: M13 Rev
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..760
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-168H12"
/clone_lib="ND-TAM"
/notes="Vector: pECBAC1; Site_1: HindIII"
BASE COUNT 171 a 187 c 139 g 263 t
ORIGIN
Query Match 15.8%; Score 79.8; DB 17; Length 760;
Best Local Similarity 77.4%; Pred. No. 7e-14;
Matches 123; Conservative 0; Mismatches 32; Indels 4; Gaps 2;

QY 98 GTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGCTGAGGTGGCGAGTTCGAATCTGCC 157
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Db 569 GTAGCTCAGCTGGTTAGAGCGGTACACTGATATGTAGAGTTCGGAGTTCGAGCTGCC 510
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QY 158 GACACCCACCAATCG---AAGGGCCATAGCTCAGCTGG-GAGAGCGCTGCTTTCACG 213
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 509 CGAGACTACTAATTGAAAAGGGGAATTAGCTCAGCTGGCTAGAGCGCTGCTTGCACG 450
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 214 CAGGAGGTCAAGGGTTCGATCCGCTGGCTCCACCAT 252
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 449 CAGGAGGTCAAGGGTTCGACTCCCTTATTCTCCACAGTT 411
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RESULT 10
BH771024
LOCUS
DEFINITION BH771024 6499 bp DNA linear GSS 01-MAY-2002
subsp. cremoris genomic, DNA sequence.
ACCESSION BH771024

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BH771024.1 GI:20373981
GSS.
Lactococcus lactis subsp. cremoris.
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
1 (bases 1 to 6499)
AUTHORS Bolotin,A., Ehrlich,S.D. and Sorokin,A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments, (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
Best homologue in strain IL1403 is ywga (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.
FEATURES
source
Location/Qualifiers
1..6499
/organism="Lactococcus lactis subsp. cremoris"
/strain="MGL1363"
/db_xref="taxon:1359"
/clone_lib="MGL1363 Random Sequence Tag Library"
/notes="Vector: PSGMU2; Site_1: SmaI; Library of
chromosomal fragments of L.lactis strain MGL1363 was
prepared by partial AluI digestion or by sonication."
BASE COUNT 1946 a 1228 c 1683 g 1642 t
ORIGIN
Query Match 13.8%; Score 69.8; DB 17; Length 6499;
Best Local Similarity 97.3%; Pred. No. 4.1e-10;
Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 175 GGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGTTCGATC 234
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Db 2165 GGGGCTTAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGTTCGATC 2224
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QY 235 CCGCTTGGCTCCA 247
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Db 2225 CCGCTAGGCTCCA 2237
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RESULT 11
BH819575
LOCUS
DEFINITION BH819575 577 bp DNA linear GSS 20-MAY-2002
BACP13-E14.Y Pristionchus pacificus BAC ends Pristionchus
pacificus genomic, DNA sequence.
ACCESSION BH819575
VERSION BH819575.1 GI:20993843
KEYWORDS GSS.
ORGANISM Pristionchus pacificus.
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 577)
AUTHORS Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R., Raddatz
,G. Witte,H., Keller,H., Kipping,I., Pires da Silva,A., Jesse,T.,
Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
TITLE A BAC-based genetic linkage map of the nematode Pristionchus
pacificus
JOURNAL Unpublished (2002)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

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FEATURES          Location/Qualifiers
  source
 1. .577
/organism="Pristionchus pacificus"
/strain="var. California"
/db_xref="taxon:54126"
/clone_lib="Pristionchus pacificus BAC ends"
BASE COUNT      129 a 142 c 139 g 167 t
ORIGIN

Query Match      13.1%; Score 66.2; DB 17; Length 577;
Best Local Similarity 89.9%; Pred. No. 1.1e-09;
Matches 71; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 172 GAAGGGCCATAGCTACGCTGGGAGAGCGCTGCTTTCACGAGGAGGTCAGCGGTTCG 231
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GACGGGCTATAGCTACGCTGGGAGAGCGCTTGCATGCTCAAGAGGTCAGCGGTTCG 60

QY 232 ATCCCGCTGGCTCCACCA 250
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Db 61 ATCCCGCTAGCTCCACCA 79

RESULT 12
AZ578476/c
LOCUS
DEFINITION
23h03 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium
sp. NGR234 genomic clone 23h03, DNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rhizobium sp. NGR234.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
REFERENCE
1 (bases 1 to 191)
AUTHORS
Viprey, V., Rosenthal, A., Broughton, W.J. and Perret, X.
TITLE
Genetic snapshots of the Rhizobium species NGR234 genome
JOURNAL
Genome Biol. 1 (6), RESEARCH0014 (2000)
MEDLINE
21114532
COMMENT
Contact: Virginie Viprey
Laboratoire de Biologie Moleculaire des Plantes Superieures
University of Geneva
1 Chemin de l'Imperatrice, Chambesy/Geneva 1292, Switzerland
Tel: +44 (0)1603450000
Fax: +44 (0)1603450045
Email: virginie.viprey@bbsrc.ac.uk
Class: shotgun.
FEATURES          Location/Qualifiers
  source
 1. .191
/organism="Rhizobium sp. NGR234"
/strain="ANU265"
/db_xref="taxon:394"
/clone="23h03"
/clone_lib="Shot-gun genomic library of Rhizobium strain
ANU265"
/notes="Vector: M13; derivative strain of NGR234 cured of
pNGR234a"
BASE COUNT      47 a 62 c 44 g 37 t 1 others
ORIGIN

Query Match      12.9%; Score 64.8; DB 17; Length 191;
Best Local Similarity 84.7%; Pred. No. 1.5e-09;
Matches 72; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 168 AATCAAGGGCCATAGCTACGCTGGGAGAGCGCTGCTTTCACGAGGAGGTCAGCGG 227
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Db 118 AACGGTTGGGCTGTAGCTACGCTGGGAGAGCACNTGCTTTGCAAGCAGGGGGTCAGCGG 59

QY 228 TTGATCCCGCTTGGCTCCACAT 252
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Db 58 TTGATCCCGCTACGCTCCACCAAT 34

RESULT 13
BH375641/c
LOCUS
DEFINITION
AG-ND-133M11.TF ND-TAM Anopheles gambiae genomic clone AG-ND-133M11
, DNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
African malaria mosquito.
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE
1 (bases 1 to 608)
AUTHORS
Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.
TITLE
Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL
Unpublished (2001)
COMMENT
Other_GSSs: AG-ND-133M11.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.
FEATURES          Location/Qualifiers
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/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-133M11"
/clone_lib="ND-TAM"
/notes="Vector: pECBAC1; Site_1: HindIII"
BASE COUNT      144 a 146 c 132 g 186 t
ORIGIN

Query Match      12.8%; Score 64.4; DB 17; Length 608;
Best Local Similarity 78.6%; Pred. No. 4.4e-09;
Matches 77; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 175 GGGCCATAGCTACGCTGGGAGAGCGCTGCTTTCACGAGGAGGTCAGCGGTTCGATC 234
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Db 561 GGGGATTAGCTACGCTGGGAGAGCACCTGCTTTGCAAGCAGGGGGTCTCGGTTCGATC 502

QY 235 CGCTTGCTCCACCATTAACCTAGTCGCCGAAAGCT 272
||| ||||| ||| ||| ||||| |||
Db 501 CGCTCATCTCCACCAAAATGATAGCGCCGAAAGGT 464

RESULT 14
BH159957/c
LOCUS
DEFINITION
BH159957 Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, DNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE
1 (bases 1 to 904)
AUTHORS
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.

```





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: February 1, 2003, 01:06:21 : Search time 1027.39 Seconds  
(without alignments)  
14135.156 Million cell updates/sec  
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Perfect score: 499  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb.ba.\*  
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4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
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26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*  
29: em.vi.\*  
30: em.htg\_hum.\*  
31: em.htg\_inv.\*  
32: em.htg\_other.\*  
33: em.htg\_mus.\*  
34: em.htg\_pln.\*  
35: em.htg\_rnd.\*  
36: em.htg\_mam.\*  
37: em.htg\_vrt.\*  
38: em.sy.\*  
39: em.htgo\_hum.\*  
40: em.htgo\_mus.\*  
41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	499	100.0	499	6	A48047	A48047 Sequence 11
2	499	100.0	499	6	AR177092	AR177092 Sequence
3	499	100.0	499	6	AX191055	AX191055 Sequence
4	329.4	66.0	530	1	PST251907	AJ251907 Pseudomon
5	327.8	65.7	530	1	PST251906	AJ251906 Pseudomon
6	304.2	61.0	560	1	AF356514	AF356514 Pseudomon
7	302.8	60.7	529	1	PST251901	AJ251901 Pseudomon
8	302.8	60.7	529	1	PST251902	AJ251902 Pseudomon
9	300.6	60.2	529	1	PST390590	AJ390590 Pseudomon
10	300.4	60.2	528	1	PST251905	AJ251905 Pseudomon
11	298.8	59.9	528	1	PST390589	AJ390589 Pseudomon
12	294.6	59.0	529	1	PST251904	AJ251904 Pseudomon
13	294.6	59.0	529	1	PST390587	AJ390587 Pseudomon
14	292.8	58.7	528	1	PST251903	AJ251903 Pseudomon
15	280.2	56.2	5785	1	PSU65012	U65012 Pseudomonas
16	276.4	55.4	544	1	AF083211	AF083211 Azotobact
17	274.2	54.9	528	1	PAE439391	AJ439391 Pseudomon
18	274.2	54.9	11176	1	AE004949	AE004949 Pseudomon
19	274.2	54.9	12065	1	AE004883	AE004883 Pseudomon
20	273.8	54.9	521	1	PAE439389	AJ439389 Pseudomon
21	272.6	54.6	471	6	A48044	A48044 Sequence 11
22	272.6	54.6	471	6	AR177089	AR177089 Sequence
23	272.6	54.6	471	6	AX191052	AX191052 Sequence
24	270.6	54.2	498	1	PAE439392	AJ439392 Pseudomon
25	270	54.1	592	1	AF422498	AF422498 Unculture
26	268.6	53.8	505	1	PST251900	AJ251900 Pseudomon
27	267.8	53.7	531	1	PAE439388	AJ439388 Pseudomon
28	266	53.3	506	1	PST390588	AJ390588 Pseudomon
29	265.4	53.2	504	6	A48046	A48046 Sequence 11
30	265.4	53.2	504	6	AR177091	AR177091 Sequence
31	265.4	53.2	504	6	AX191054	AX191054 Sequence
32	265.4	53.2	505	1	PST251910	AJ251910 Pseudomon
33	265.4	53.2	505	1	PST390583	AJ390583 Pseudomon
34	265.4	53.2	505	1	PST390584	AJ390584 Pseudomon
35	265.2	53.1	523	1	PST390581	AJ390581 Pseudomon
36	265	53.1	505	1	PST390585	AJ390585 Pseudomon
37	264.8	53.1	538	1	AF083212	AF083212 Azotobact
38	263.4	52.8	505	1	PST390582	AJ390582 Pseudomon
39	261.6	52.4	660	1	PSDFC	L28150 Pseudomonas
40	261.4	52.4	490	1	PAE439390	AJ439390 Pseudomon
41	261.2	52.3	506	1	PST251908	AJ251908 Pseudomon
42	261.2	52.3	659	1	PSDFFA	L28148 Pseudomonas
43	260.4	52.2	533	1	AF079808	AF079808 Azotobact
44	258	51.7	659	1	PSDFB	L28149 Pseudomonas
45	252.4	50.6	477	1	PST251909	AJ251909 Pseudomon

ALIGNMENTS

RESULT 1  
A48047  
LOCUS A48047  
DEFINITION Sequence 114 from Patent WO9600298.  
ACCESSION A48047  
VERSION A48047.1 GI:2301909  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 499)  
AUTHORS James C. Rees, R. and Van H. H.  
TITLE SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF  
EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY  
JOURNAL Patent: WO 9600298-A 114 04-JAN-1996;

linear PAT 07-MAR-1997

INNOGENETICS NV (BE)  
Other publication AU 2924695 960119.

FEATURES	SOURCE
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BASE COUNT	123 a	109 c	130 g	137 t
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Query Match	100.0%	Score 499;	DB 6;	Length 499;
Best Local Similarity	100.0%	Pred. No. 3.9e-130;		
Matches 499;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

**QY** 1 ATCGAAGACTTCAGCTTCTTCATAGTTCACACACGAATTGCTTGATTCACCTTGGGAAAA 60  
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**Db** 1 ATCGAAGACTTCAGCTTCTTCATAGTTCACACACGAATTGCTTGATTCACCTTGGGAAAA 60

Db  
61 GCGATTGGGTTGAGACCCGAGAGTGACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120

Qv  
121 CCCGTATAAGGTCAGSTCGSCAGTTCGAATCTGCCCACACCCCACCAATCTCTCCGCATC 180

Accession	Sequence	Length
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Qy	181 GCCAGTGTCAAATGGGGCCCATAGCTCAGCTGGGAGAGCGCCCTCTTTGCACGCAGGAGGT	240

QY 241 CAGGAGTTTCGATCCTCTCTGGGCTCCACCATCAACTCAGGATCGCTGAAAGCTCAGAAATG 300  
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241 CAGGAGTTTCGATCCTCTCTGGGCTCCACCATCAACTCAGGATCGCTGAAAGCTCAGAAATG 300  
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Qy	301 AACATTGGTAGTTCAAATGTTGATTCTTGCTTTGGCCAGAACTGTTCTTTAAAAATTT	360
Db	301 AACATTGGTAGTTCAAATGTTGATTCTTGCTTTGGCCAGAACTGTTCTTTAAAAATTT	360

301 GGGTATGTGATACAAAGTGACTAACAGCGTGTTCACTGCACGTGTTTAAATCAAGGCAAAA 420  
 361 GGGTATGTGATACAAAGTGACTAACAGCGTGTTCACTGCACGTGTTTAAATCAAGGCAAAA 420

Db	421	TTTGGGAGTTC	AAGCGCGAATTTTCGGCGG	AATGTCGCTTCAGGTTACGAATCTATAACC	480
Qy	481	AGATTGCTTGGGGTTATAT			499

Db 481 AGATTGCTTGGGTTATAT 499

RESULT 2

LOCUS	AR177092	499 bp	DNA	linear	PAT 17-DEC-2001
DEFINITION	Sequence	114	from patent	US 6312903.	
ACCESSION	AR177092				
VERSION	AR177092.1				

SOURCE	ORGANISM
Unknown.	Unknown.
Unknown.	Unknown.
Unknown.	Unclassified.

**TITLE** Simultaneous detection, identification and differentiation of eubacterial taxa using a hybridization assay

source	i..499	/organism="unknown"
BASE COUNT	123 a	109 c 130 g
ORIGIN		137 t

Query Match	100.0%;	Score 499;	DB 6;	Length 499;
Best Local Similarity	100.0%;	Pred. No. 3.9e-130;		

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Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	ATCGAAGACGCTTCAGCTTCTTCATTAAGTTCCCAACACGAATTGCTTGATTCACTTGGAAAA	60
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Db	1	ATCGAAGACGCTTCAGCTTCTTCATTAAGTTCCCAACACGAATTGCTTGATTCACTTGGAAAA	60

Qy	61	GC	GATTGGGTTGAGACCCGAGAGTGACGATTGGTCTGTAGCTCAGTTGGTTAGACGCCA	120
Dh	61	GC	GATTGGGTTGAGACCCGAGAGTGACGATTGGTCTGTAGCTCAGTTGGTTAGACGCCA	120

Db	61	CGCATTTGGGTTGAGACCCCGAGAGTACGATTTGGTCTGTGACTCAGTTGGTTAGACGCCA	120
QY	121	CCCCTGATAAGGGTGAGGTCGGCAGTTCGAATCTGCCAGACCCACCAATTGTCGGGATG	180

QY	181	GCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGGCTGCTTTGCACGCAGGAGGT	240
Dh	181	GCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGGCTGCTTTGCACGCAGGAGGCT	240

Accession	Gene	Accession	Gene
QY 241	CAGGAGTTCGATCCCTCTGGCTCCACCATCAACTCAGGATCGCTGAAAGCTCAGAAATG 300	Db 241	CAGGAGTTCGATCCCTCTGGCTCCACCATCAACTCAGGATCGCTGAAAGCTCAGAAATG 300

Db 301 AACATTGGTAGTTCAAATGTTGATTCTGGTCTTTGGCCAGACATGTTCTTTAAAAATTT 360

Db	361	GGGATGTGATGAAAGTGACTACACGCGTGTTCCTACTGACGTTGTTAATCAAGGCAAA	420
QY	421	TTTCGCGATTCAAGCCGGAATTTTCGGCGGAATGTCGTCTTCACGTTACGAATCTATAACC	480

DB	4 21	481	499	480
QY	TTTGGCGATTC	AGATTGCTT	GGGGTTATAT	TTCACGTTACGAATCTATAACC

RESULT 3  
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DEFINITION Sequence 114 from Patent EP1091004.  
ACCESSION AX191055  
VERSION AX191055.1 GI:15149700  
KEYWORDS

ORGANISM	unidentified unclassified.
REFERENCE	1 (bases 1 to 499)

**JOURNAL**

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QY 361 GGGTATGTGATAGAAGTGAATAACAGCGTGTCTTCACTGCACGTTGTTTAATCAAGGCAAAA 420
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QY 421 TTGCGAGTTCAAGCGGGAATTTTCGGCGAATGTCGTCCTTCAAGTACGATCTATAACC 480
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Db 481 AGATTGCTTGGGGTTATAT 499

RESULT 4
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LOCUS Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), rRNA-1le
DEFINITION AJ251907
ACCESSION AJ251907.1 GI:9844595
VERSION Internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer
KEYWORDS rRNA-1le; tRNA-Ala; tRNA-1le.
SOURCE Pseudomonas stutzeri.
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE 1 (bases 1 to 530)
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
MEDLINE 20393664
PUBMED 10939670
REFERENCE 2 (bases 1 to 530)
AUTHORS Bannasar,A.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
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DEFINITION AJ251906
ACCESSION AJ251906.1 GI:9844594
VERSION Internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer
KEYWORDS rRNA-1le; tRNA-Ala; tRNA-1le.
SOURCE Pseudomonas stutzeri.
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE 1 (bases 1 to 530)
AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bannasar,A.
TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for
the definition of Pseudomonas stutzeri genomovars and other
Pseudomonas species
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)
MEDLINE 20393664
PUBMED 10939670
REFERENCE 2 (bases 1 to 530)
AUTHORS Bannasar,A.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1999) Bannasar A., Division of Microbiology,
National Research Centre for Biotechnology, Mascheroder Weg 1,
D-38124 Braunschweig, GERMANY
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RNA-Ile; trna-Ala gene; trna-Ile gene.  
Pseudomonas stutzeri.  
Pseudomonas stutzeri.  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.

1 (bases 1 to 529)  
Guasp,C., Moore,E.R., Lalucat,J. and Bannas,A.  
Utility of internally transcribed 16S-23S rDNA spacer regions for  
the definition of Pseudomonas stutzeri genomovars and other  
Pseudomonas species  
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)

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2 (bases 1 to 529)  
Bannas,A.  
Direct Submission  
Submitted (14-DEC-1999) Bannas A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascheroder Weg 1,  
D-38124 Braunschweig, GERMANY

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QY 236 GAGTCAGGAGTTCGATCTCTTGGTCCACCATCA--ACTCAGCATCGCTGAAGAGCTC 293

RNA-Ile; trna-Ala gene; trna-Ile gene.  
Pseudomonas stutzeri.  
Pseudomonas stutzeri.  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.

1 (bases 1 to 529)  
Guasp,C., Moore,E.R., Lalucat,J. and Bannas,A.  
Utility of internally transcribed 16S-23S rDNA spacer regions for  
the definition of Pseudomonas stutzeri genomovars and other  
Pseudomonas species  
Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)

20393664  
10939670  
2 (bases 1 to 529)  
Bannas,A.  
Direct Submission  
Submitted (14-DEC-1999) Bannas A., Division of Microbiology,  
National Research Centre for Biotechnology, Mascheroder Weg 1,  
D-38124 Braunschweig, GERMANY

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QY 405 GTT--AATCAAGGCAAAATTTCCGAGTT-----CAAGCCGGAATTTTCGGCGAA 451  
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QY	121	CCCTGTATAAGGGTGGAGTTCGAGTTCGAATCTGCCAGACCCACCAATTGTC-----G	CCCTGTATAAGGGTGGAGTTCGAGTTCGAATCTGCCAGACCCACCAATTGTC-----G
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QY	176	GGATGCCAGTGTCAAAATGGGCGCATAGCTCAGCTGGGAGAGCGCTTTCGACGCGAG	GGATGCCAGTGTCAAAATGGGCGCATAGCTCAGCTGGGAGAGCGCTTTCGACGCGAG
Db	182	TGTGGCCGATCTGTAGATGGGCGCATAGCTCAGCTGGGAGAGCGCTTTCGACGCGAG	TGTGGCCGATCTGTAGATGGGCGCATAGCTCAGCTGGGAGAGCGCTTTCGACGCGAG
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Db	482	TGTCGCTTCACGTTA-TAGACAGTAACAGATTGCTTGGGTTATAT	TGTCGCTTCACGTTA-TAGACAGTAACAGATTGCTTGGGTTATAT
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LOCUS		and tRNA-Ala, strain AN10.	
DEFINITION			
ACCESSION		AJ251904	
VERSION		AJ251904.1 GI:9844592	
KEYWORDS		Internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer RNA-Ile; tRNA-Ala; tRNA-Ile.	
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ORGANISM		Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.	

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QY	176	GGATGCCAGTGTCAAAATGGGCGCATAGCTCAGCTGGGAGAGCGCTTTCGACGCGAG	GGATGCCAGTGTCAAAATGGGCGCATAGCTCAGCTGGGAGAGCGCTTTCGACGCGAG
Db	182	TGTGGCCGATCTGTAGATGGGCGCATAGCTCAGCTGGGAGAGCGCTTTCGACGCGAG	TGTGGCCGATCTGTAGATGGGCGCATAGCTCAGCTGGGAGAGCGCTTTCGACGCGAG
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QY	452	TGTCGCTTCACGTTACGATCTATAACAGATTGCTTGGGTTATAT	TGTCGCTTCACGTTACGATCTATAACAGATTGCTTGGGTTATAT
Db	482	TGTCGCTTCACGTTA-TAGACAGTAACAGATTGCTTGGGTTATAT	TGTCGCTTCACGTTA-TAGACAGTAACAGATTGCTTGGGTTATAT
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PST390589		Pseudomonas stutzeri intergenic spacer, tRNA-Ile and tRNA-Ala	
LOCUS		genes, strain Pili.	
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ACCESSION		AJ390589	
VERSION		AJ390589.1 GI:9844770	
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SOURCE		Pseudomonas stutzeri.	
ORGANISM		Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.	
REFERENCE		1 (bases 1 to 528)	
AUTHORS		Guasp,C., Moore,E.R., Lalucat,J. and Bennisar,A.	
TITLE		Utility of internally transcribed 16S-23S rDNA spacer regions for the definition of Pseudomonas stutzeri genomovars and other Pseudomonas species	
JOURNAL		Pseudomonas species	
MEDLINE		Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)	
PUBMED		20393664	
REFERENCE		2 (bases 1 to 528)	
AUTHORS		Bennisar,A.	
TITLE		Direct Submission	
JOURNAL		Submitted (15-DEC-1999) Bennisar A., Division of Microbiology, National Research Centre for Biotechnology, Mascheroder Weg 1,	

REFERENCE 1 (bases 1 to 529)  
 AUTHORS Guasp,C., Moore,E.R., Lalucat,J. and Bennasar,A.  
 TITLE Utility of internally transcribed 16S-23S rDNA spacer regions for  
 the definition of pseudomonas stutzeri genomovars and other  
 Pseudomonas species  
 JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)  
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 PUBMED 10939670  
 REFERENCE 2 (bases 1 to 529)  
 AUTHORS Bennasar,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-DEC-1999) Bennasar A., Division of Microbiology,  
 National Research Centre for Biotechnology, Mascheroder Weg 1,  
 D-38124 Braunschweig, GERMANY

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 QY 236 GAGGTCAGAGTTGATCCTCTTGGCTCCACCATCA--ACTCAGCATGCTGAAAGCTC 293  
 Db 242 GAGGTCAGCGGTTGATCCCGCTTGGCTCCACCATTATTCGCACAATCGCTGAAAGCTC 301  
 QY 294 AGAATGAACATTGGTAGTTC-----ANGTTGATTTCGTGCTCTTGC 336  
 Db 302 AGAATGAGTCTGCTGCTCGCATCCTTTGATGTGAGGGTATTGATTTCTGCTCTTTCG 361  
 QY 337 GCAGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAGTACTACAGCG---TGTTT 393  
 Db 362 GCCAGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAGTACTGATTTGAGTGGTCACTTT 421  
 QY 394 CACTGCAGTTGTT--AATCAAGCAAAATTTGCGAGTTC--AAGCGCAATTTTCGGCGA 450  
 Db 422 CACTGGTGATTATTCAAGTCAAGTAAAAATTTGCGTGTTCTCTATGCAATTTTCGGCGA 481  
 QY 451 ATGTCGCTCTCACTGTACGATCTATAACACGATTGCTTGGGGTTATAT 499  
 Db 482 ATGTCGCTCTCAAGTTA--TAGACAGTAAACAGATTGCTTGGGGTTATAT 529

RESULT 13	PST390587	529 bp	DNA	linear	BCT 16-AUG-2000
LOCUS	Pseudomonas stutzeri intergenic spacer, tRNA-Ile and tRNA-Ala genes, strain AER5.1.				
DEFINITION					
ACCESSION	AJ390587.1	GI:9844760			
VERSION					
KEYWORDS	IGS; intergenic spacer; transfer RNA Ile; transfer RNA-Ala; tRNA-Ala gene; tRNA-Ile gene.				
SOURCE	Pseudomonas stutzeri.				
ORGANISM	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.				
REFERENCE	1 (bases 1 to 529)				
AUTHORS	Guasp,C., Moore,E.R., Lalucat,J. and Bennasar,A.				
TITLE	Utility of internally transcribed 16S-23S rDNA spacer regions for the definition of Pseudomonas stutzeri genomovars and other Pseudomonas species				
JOURNAL	Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)				
MEDLINE	20393664				
PUBMED	10939670				
REFERENCE	2 (bases 1 to 529)				
AUTHORS	Bennasar,A.				
TITLE	Direct Submission				
JOURNAL	Submitted (15-DEC-1999) Bennasar A., Division of Microbiology, National Research Centre for Biotechnology, Mascheroder Weg 1, D-38124 Braunschweig, GERMANY				
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	/db_xref="taxon:316"				
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	/note="codon recognized: AUC"				
anticodon	(pos:127..129,aa:Ile)				
	201..275				
	/product="tRNA-Ala"				
	/note="codon recognized: GCA"				
	/anticodon=(pos:228..230,aa:Ala)				
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ORIGIN					
Query Match	59.0%;	Score	294.6;	DB 1;	Length 529;
Best Local Similarity	82.0%;	Pred. No.	2.3e-72;		
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				Indels	31;
				Gaps	7;
QY	1	ATCGAAGACTTCAGCTCTTCATAGTTCCACACGAATTCGTTCAATTCACCTGGGAAAA	60		
Db	2	ATCGAAGACTTCAGCTCTTCATAGTCTCCACACGAATTCGTTCAATTCACCTAGCGAAAA	61		
QY	61	GCATTGGGTTGAGACCCGAGAGTGACGATTGGGTCGTAGCTCAGTTGGTTAGAGCGCA	120		
Db	62	GCATTGGGTTGACCCGAGAGACGATTGGGTCGTAGCTCAGTTGGTTAGAGCGCA	121		
QY	121	CCCTCATAGGTTGAGTTCGCGAGTTCGAATCTGCCAGACCCACCAATTTGTC-----G	175		
Db	122	CCCTCATAGGTTGAGTTCGCGAGTTCGAATCTGCCAGACCCACCAATTTGTCATGGGA	181		
QY	176	GGATGCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGCTCTTTGCACCGAG	235		
Db	182	TGTGCCGATCTGTAGATGGGCCATAGCTCAGCTGGGAGAGCGCTCTTTGCACCGAG	241		
QY	236	GAGGTTCAGGATTCGATCCTCTTGGCTCCACCATCA--ACTCACGATTCGCTGAAAGCT	293		
Db	242	GAGGTTCAGGATTCGATCCTCTTGGCTCCACCATCAATTCGACATTCGCTGAAAGCT	301		
QY	294	AGAAATGAACATTGGTAGTTCA-----ATGTTGATTTCTGGCTTTTGC	336		
Db	302	AGAAATGAGTCTGCTCTTCGATCCTTTGATGTGTGAGGGTATTGATTCTGCTTTTGC	361		



QY	337	GCAGAACTGTTCTTAAATAATTTGGGTATGTGATAGAGTCACTAACAGCG--TGTGTT	393
Db	362	GCAGAACTGTTCTTAAATAATTTGGGTATGTGATAGAGTCACTAACAGCG--TGTGTT	421
QY	394	CAGTCAGCAGTTGTT--AATCAAGGCAAAATTTGCGAGTTC-AAGCGGAAATTTTCGGCGA	450
Db	422	CAGTCAGCAGTTGTT--AATCAAGGCAAAATTTGCGAGTTC-AAGCGGAAATTTTCGGCGA	481
QY	451	ATGTCGCTCTCAGTTACCAATCTATACCAAGTTCGTTGGGGTTATAT	499
Db	482	ATGTCGCTCTCAGTTA-TAGACAGTAAACAGATTGCTTGGGGTTATAT	529
RESULT	14		
PSU65012		528 bp DNA linear BCT 16-AUG-2000	
LOCUS		Pseudomonas stutzeri internal transcribed spacer 1 (ITS1), tRNA-Ile	
DEFINITION		and tRNA-Ala, strain DSM 50227.	
ACCESSION		AJ251903	
VERSION		1.1	
KEYWORDS		internal transcribed spacer 1; ITS1; transfer RNA-Ala; transfer RNA-Ile; tRNA-Ala; tRNA-Ile.	
SOURCE		Pseudomonas stutzeri.	
ORGANISM		Pseudomonas stutzeri Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	
REFERENCE		1 (bases 1 to 528)	
AUTHORS		Quispel, C., Moore, E.R., Lalucat, J. and Bannasch, A.	
TITLE		Utility of internally transcribed 16S-23S rDNA spacer regions for the definition of Pseudomonas stutzeri genomovars and other Pseudomonas species	
JOURNAL		Int. J. Syst. Evol. Microbiol. 50 Pt 4, 1629-1639 (2000)	
MEDLINE		20393664	
PUBMED		10939670	
REFERENCE		2 (bases 1 to 528)	
AUTHORS		Bannasch, A.	
TITLE		Direct Submission	
JOURNAL		Submitted (14-DEC-1999) Bannasch A., Division of Microbiology, National Research Centre for Biotechnology, Mascheroder Weg 1, D-38124 Braunschweig, GERMANY	
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tRNA		201..275	
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BASE COUNT		124 a 111 c 143 g 150 t	
ORIGIN			
Query Match		58.7%; Score 292.8; DB 1; Length 528;	
Best Local Similarity		80.7%; Pred. No. 7.4e-72;	
Matches 426; Conservative		0; Mismatches 72; Indels 30; Gaps 6;	
QY	1	ATCGAAGACTTCAGCTTCTTCAATAGTCCACACGAATTCCTTATTCACCTTCGGA	60
Db	2	ATCGAAGACTTCAGCTTCTTCAATAGTCCACACGAATTCCTTATTCACCTTCGGA	61
QY	61	CGATTTGGGTTGAGACCCGAGAGTGGGTCTGTAGTCTGAGTGGTGTAGAGCGCA	120
Db	62	CGATTTGGGTTGAGACCCGAGAGTGGGTCTGTAGTGGTGTAGAGCGCA	121
QY	121	CCCTGATAAGGGTGAAGTTCGCGAGTTCGAATCTGCCACAGCCCAATTCCTC	175
Db	122	CCCTGATAAGGGTGAAGTTCGCGAGTTCGAATCTGCCACAGCCCAATTCCTC	181
QY	176	GGATGGCAGTGTCAAAATGGGGCCATAGCTAGCTGGGAGAGCGCTTCACGCGAG	235
Db	182	TGTGGCGATCTGTAGATGGGGCCATAGCTAGCTGGGAGAGCGCTTCACGCGAG	241
QY	236	GAGTCAGGAGTTCGATCCCTCTTGGCTCCACCAATCACTC-ACGATCGCTGAAAGCTCA	294
Db	242	GAGTCAGGAGTTCGATCCCTCTTGGCTCCACCAATCACTC-ACGATCGCTGAAAGCTCA	301
QY	295	GAATGAAACATTTGGTAGTTCA-----ATGTTGATTTCTGGTCTTTGGCG	337
Db	302	GAATGAGTGTCTTGGCATCTCTGTGATGTGAGGGTATTGATTTCTGGTCTTTGGCG	361
QY	338	CCAGAACTGTTCTTTAAATAATTTGGGTATGTGATAGAGTCACTAACAGCGTGTTC	397
Db	362	CCAGAACTGTTCTTTAAATAATTTGGGTATGTGATAGAGTCACTAACAGCGTGTTC	421
QY	398	GCAGCTGTTTAAATCAAGGCAA-----AATTTGCGAGTTC-AAGCGGAAATTTTCGGG	451
Db	422	ACTGTCGATTTTAAATCAAGGCAA-----AATTTGCGAGTTC-AAGCGGAAATTTTCGGG	481
QY	452	TGTCGCTCTCAGTTACGAATCTATACCAAGTTCGTTGGGGTTATAT	499
Db	482	TGTCGCTCTCAGTTA-TAGACAGTAAACAGATTGCTTGGGGTTATAT	528
RESULT	15		
PSU65012		5785 bp DNA linear BCT 11-DEC-1996	
LOCUS		Pseudomonas stutzeri 16S rRNA, 23S rRNA, 5S rRNA, tRNA-Ile, and tRNA-Ala genes, complete sequences.	
DEFINITION		tRNA-Ala genes, complete sequences.	
ACCESSION		U65012	
VERSION		1.1	
KEYWORDS		GI:1718243	
SOURCE		Pseudomonas stutzeri.	
ORGANISM		Pseudomonas stutzeri Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	
REFERENCE		1 (bases 1 to 5785)	
AUTHORS		Kerkhof, L.	
TITLE		A ribosomal RNA operon from Pseudomonas stutzeri	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 5785)	
AUTHORS		Kerkhof, L.	
TITLE		Direct Submission	
JOURNAL		Submitted (24-JUL-1996) Inst. Mar. Coastal. Sci., Rutgers University, 15 Dudley Rd., New Brunswick, NJ 08903, USA	
COMMENT		On Dec 11, 1996 this sequence version replaced gi:1513132.	
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		/note="codon recognized: AUC"	
		2180..2255	
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rRNA 5540..5674
BASE COUNT 1513 a 1241 c 1732 g 1287 t 12 others
ORIGIN

Query Match 56.2%; Score 280.2; DB 1; Length 5785;
Best Local Similarity 80.0%; Pred. No. 3.2e-68;
Matches 421; Conservative 0; Mismatches 78; Indels 27; Gaps 7;

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Db 1984 ATCGAAGACTTCAGCTTCTTCATAAGTTCCACACGAATGCTTGATTCACCTGCCGAAAA 2043
QY 61 GCGATTGGGTTGAGACCCGAGAGTAGCGATTGGGTCTGTAGTCAGTTGTTAGAGCGCA 120
Db 2044 GCGATTGGGTTGAGACCCGAGAGTAGCGATTGGGTCTGTAGTCAGTTGTTAGAGCGCA 2103
QY 121 CCCTGATAGGGTGAAGTCCGGAGTTTCAATCTGCCAGACCCCAACAATTGTCTGGGA 2163
Db 2104 CCCTGATAGGGTGAAGTCCGGAGTTTCAATCTGCCAGACCCCAACAATTGTCTGGGA 2163
QY 177 GATGGCCAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCGCTTGCTTGACGCAGG 236
Db 2164 TGTGGCGATCTGTAGATGGCCATAGCTCAGCTGGGAGAGCGCTTGCTTGACGCAGG 2223
QY 237 AGGTCAGGAGTTCGATCCTCTGGCTCCACCATCA--ACTCAGATCGCTGAAAG-CTC 293
Db 2224 AGGTCAGGAGTTCGATCCTCTGGCTCCACCATCA--ACTCAGATCGCTGAAAG-CTC 293
QY 294 AGAATGAACATGGTA-----GTTCAATGTTGATTTCTTGCTTTGGCCAGACTGT 347
Db 2284 AGAATGAACATGGTA-----GTTCAATGTTGATTTCTTGCTTTGGCCAGACTGT 2343
QY 348 TCCTTTAAATAATTGGGTATGTCATAGAGTGAAT---AACAGCGTGTTCACCTGCACGTT 404
Db 2344 TCCTTTAAATAATTGGGTATGTCATAGAGTGAAT---AACAGCGTGTTCACCTGCACGTT 2403
QY 405 GTTAA--TCAGGCAAAATTTGCGAGTTCAA-----GCGCGAATTTTCGGCGAATG 453
Db 2404 ATTCAGTCAAGGTAAATTTGCGAGTTGCTCGAGAGAGCGAATNGATTTNNNCGAATN 2463
QY 454 TCGTCTTCACGTTACGAATCTATAACAGATTGCTTGGGGTTATAT 499
Db 2464 TCGTCTTCACGTTATAGACAGTAACACAGATTGCTTGGGGTTATAT 2509
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Job time : 1032.39 secs

GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 19:23:36 : Search time 118.163 Seconds  
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Title: US-09-931-486-114

Perfect score: 499

Sequence: 1 ATCGAAGACTTCAGCTCTT.....CAGATTGCTTGGGGTTATAT 499

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	499	100.0	499	17 AAT11845	P. alcaligenes LMG
2	272.6	54.6	471	17 AAT11842	P. aeruginosa UZG
3	265.4	53.2	504	17 AAT11844	P. stutzeri LMG 23
4	198.4	39.8	468	17 AAT11846	P. putida LMG 2232
5	193.2	38.7	520	17 AAT11843	P. psedocalligene
6	158.6	31.8	588	22 AAI69774	16S/23S rRNA spacer
7	108.8	21.8	470	17 AAT11898	Yersinia enterocol
c 8	106	21.2	2839	22 AAH54998	S. epidermidis gen
9	106	21.2	3444	22 AAH54992	S. epidermidis gen

10	106	21.2	4429	22 AAH54300	S. epidermidis gen
11	105.6	21.2	1396	22 AAH55089	S. epidermidis gen
12	102.4	20.5	400	18 AAV78022	Staphylococcus aur
c 13	102.4	20.5	400	18 AAV77902	Staphylococcus aur
14	102.4	20.5	1311	18 AAV77852	Staphylococcus aur
c 15	99.8	20.0	400	18 AAV77984	Staphylococcus aur
16	99	19.8	463	17 AAT11870	Listeria-like isol
17	99	19.8	475	17 AAT11869	Listeria-like isol
18	98.8	19.8	640681	24 ABA92787	Buchnera sp. genom
c 19	98.2	19.7	351	18 AAV78405	Staphylococcus aur
20	97.2	19.5	582	12 AAQ14104	B.pertussis ATCC 1
21	97.2	19.5	590	12 AAQ14105	B.bronchiseptica N
22	96.2	19.3	249	17 AAT11855	A. haemolyticus LM
23	96	19.2	5097	20 AAX24983	E. coli MG1655 rrr
c 24	96	19.2	5341	20 AAX24986	E. coli MG1655 rrr
25	95.2	19.1	808	17 AAT11889	Brucella melitensi
26	95.2	19.1	808	17 AAT11890	Brucella suis NIDO
27	95.2	19.1	809	17 AAT11891	Brucella abortus
28	92.8	18.6	5105	20 AAX24989	E. coli MG1655 rrr
c 29	92	18.4	243	23 AAS48781	Staphylococcus aur
c 30	91.4	18.3	255	23 AAS48800	Staphylococcus aur
c 31	91.4	18.3	255	23 AAS48825	Staphylococcus aur
c 32	91.4	18.3	255	23 AAS48838	Staphylococcus aur
c 33	91.4	18.3	255	23 AAS48846	Staphylococcus aur
c 34	91.4	18.3	255	23 AAS48854	Staphylococcus aur
c 35	91.4	18.3	255	23 AAS48877	Staphylococcus aur
c 36	91.4	18.3	255	23 AAS48882	Staphylococcus aur
c 37	91.4	18.3	255	23 AAS48896	Staphylococcus aur
c 38	91.4	18.3	255	23 AAS48898	Staphylococcus aur
c 39	91.4	18.3	255	23 AAS48967	Staphylococcus aur
c 40	91.4	18.3	255	23 AAS49061	Staphylococcus aur
c 41	89.4	17.9	2944528	24 ABA03041	Listeria monocytog
c 42	89.2	17.9	363	17 AAT11865	L. ivanovii CIP 78
43	88.4	17.7	343	18 AAV78492	Staphylococcus aur
44	88.2	17.7	591	21 AAS39330	Z. raiffosivorans
c 45	87.8	17.6	400	18 AAV77919	Staphylococcus aur

## ALIGNMENTS

## RESULT 1

AAT11845  
ID AAT11845 standard; DNA; 499 BP.  
AC AAT11845;  
XX AAT11845;  
DT 03-SEP-1996 (first entry)  
XX  
XX  
DE P. alcaligenes LMG 1224 16S-23S rRNA spacer region.  
XX  
XX  
KW Probe: detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.  
XX  
XX Pseudomonas alcaligenes.  
XX  
XX WO9600298-A1.  
XX  
PD 04-JAN-1996.  
XX  
XX 23-JUN-1995; 95WO-EP02452.  
XX  
PR 07-APR-1995; 95EP-0870032.  
PR 24-JUN-1994; 94EP-0870106.  
XX  
XX (INNO-) INNOGENETICS NV.  
XX  
XX Jannes G, Rossau R, Van Heuverswyn H;  
XX WPI; 1996-068882/07.  
XX  
XX Novel hybridisation assay for the detection of eubacteria - esp

PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
XX  
PS Claim 2; Fig 39; 248pp; English.  
XX  
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
CC regions derived from various microorganisms. These sequences were  
CC used in the method of the invention for the detection and identification  
CC of at least one or more microorganisms. The method comprises amplifying  
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
CC given in AAT34011-77 to the amplified sequence. These probes were  
CC specifically used to detect microorganisms in samples originating from  
CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
CC *aeruginosa* LMG 1324.  
XX  
SQ Sequence 499 BP; 123 A; 109 C; 130 G; 137 T; 0 other;  
Query Match 100.0%; Score 499; DB 17; Length 499;  
Best Local Similarity 100.0%; Pred. No. 1.5e-158;  
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAATTCGTTGATTCACCTTCGCAAAA 60  
Db 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAATTCGTTGATTCACCTTCGCAAAA 60  
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QY 181 GCCAGTGTCAAAATGGGSCCATAGCTCAGCTGGGAGAGCGCTTTCACGACGAGGAGT 240  
Db 181 GCCAGTGTCAAAATGGGSCCATAGCTCAGCTGGGAGAGCGCTTTCACGACGAGGAGT 240  
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QY 301 AACATTGGTGTAGTCAATGTGTTGTTCTGTTGGCCAGAACTGTCTTTAAATAATTT 360  
Db 301 AACATTGGTGTAGTCAATGTGTTGTTCTGTTGGCCAGAACTGTCTTTAAATAATTT 360  
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QY 421 TTTCGAGTTCAGCGGGAATTTTCGGCGAATGTCGTTCTTCAGTTACGATCTATAAC 480  
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QY 481 AGATTGCTTGGGTTATAT 499  
Db 481 AGATTGCTTGGGTTATAT 499  
RESULT 2  
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AC AAT11842 standard; DNA; 471 BP.  
XX AAT11842;  
XX  
DT 03-SEP-1996 (first entry)  
XX  
DE *P. aeruginosa* UZG 5669 16S-23S rRNA spacer region.  
XX  
KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; respiratory tract; universal;  
KW species-specific; ss.  
XX  
OS *Pseudomonas aeruginosa*.  
XX

PN W09600298-A1.  
XX  
PD 04-JAN-1996.  
XX  
PF 23-JUN-1995; 95WO-EP02452.  
XX  
PR 07-APR-1995; 95EP-0870032.  
PR 24-JUN-1994; 94EP-0870106.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Jannes G, Rossau R, Van Heuverswyn H;  
XX  
DR WPI; 1996-068882/07.  
XX  
PT Novel hybridisation assay for the detection of eubacteria - esp  
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
XX  
PS Claim 2; Fig 36; 248pp; English.  
XX  
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer  
CC regions derived from various microorganisms. These sequences were  
CC used in the method of the invention for the detection and identification  
CC of at least one or more microorganisms. The method comprises amplifying  
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes  
CC given in AAT34011-77 to the amplified sequence. These probes were  
CC specifically used to detect microorganisms in samples originating from  
CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
CC *aeruginosa* UZG 5669.  
XX  
SQ Sequence 471 BP; 116 A; 103 C; 120 G; 132 T; 0 other;  
Query Match 54.6%; Score 272.6; DB 17; Length 471;  
Best Local Similarity 80.7%; Pred. No. 7.5e-82;  
Matches 409; Conservative 0; Mismatches 54; Indels 44; Gaps 6;  
QY 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAATTCGTTGATTCACCTTCGCAAAA 60  
Db 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAATTCGTTGATTCACCTTCGTTA-- 57  
QY 61 GCATTTGGTGTAGACCCGAGAGTACGATGGGTCTGTAGTCAGTTCGTTAGAGCGCA 120  
Db 58 -----GACGATGGGTCTGTAGTCAGTTCGTTAGAGCGCA 93  
QY 121 CCCTGATAGAGGTGAGTGGCGAGTTCGAATCTGCCACACCCACCAATTCGCGGATG 180  
Db 94 CCCTGATAGAGGTGAGTGGCGAGTTCGAATCTGCCACACCCACCAATTCGTTGTTG 153  
QY 181 GCAGTGTG---TCAAAATGGGSCCATAGCTCAGCTGGGAGAGCGCTGTTTCAGCGCAGGA 237  
Db 154 CTGCGTGTATCCGATACGGGSCCATAGCTCAGCTGGGAGAGCGCTGTTTCAGCGCAGGA 213  
QY 238 GGTACAGAGTTCGATCCTCTGCTCCACCATCACTCAGATCGCTGAAGCTCAGAA 297  
Db 214 GGTACAGAGTTCGATCCTCTGCTCCACCATCTA-AAACAATGTCGAAGCTCAGAA 272  
QY 298 ATGAACATTTGGTGTAGTCAATGTTGATTCGTTGCTTTCGCCAGAACTGTTCTTTAAAAA 357  
Db 273 ATGAATGTTGTTGATGAACATTCGTTGCTTTCGCCAGAACTGTTCTTTAAAAA 332  
QY 358 TTTGGGTATGTATAGTAAGTGA---CTAACAGCGTGTTCACCTGCAGCTGTTGTT--AATCA 412  
Db 333 TTCGGGTATGTATAGTAAGTGAAGTGAATGATCTCTTTTCACCTGGTGTATCATCAAGTCA 392  
QY 413 AGGCAAAATTTGGGAGTTCAGCGGAAATTTTCGGCGAATGTCGTTCTTCACGTTACCAAT 472  
Db 393 AGGTAATTTGGGAGTTCAGCGGAAATTTTCGGCGAATGTCGTTCTTCAC-----A 444  
QY 473 CTATAACAGATTCGTTGGGTTATAT 499  
Db 445 GTATAACAGATTCGTTGGGTTATAT 471

```

RESULT 3
AAT11846
ID AAT11844 standard; DNA; 504 BP.
XX
AC AAT11844;
XX
DT 03-SEP-1996 (first entry)
XX
DE P. stutzeri LMG 2333 16S-23S rRNA spacer region.
XX
KW Probe; detection; identification; microorganism; amplify;
KW 16S-23S rRNA spacer region; respiratory tract; universal;
KW species-specific; ss.
XX
OS Pseudomonas stutzeri.
XX
PN WO9600298-Al.
XX
PD 04-JAN-1996.
XX
PF 23-JUN-1995; 95WO-EP02452.
XX
PR 07-APR-1995; 95EP-0870032.
XX
PR 24-JUN-1994; 94EP-0870106.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Jannes G, Rossau R, Van Heuverswyn H;
XX
DR WPI; 1996-068882/07.
XX
PT Novel hybridisation assay for the detection of eubacteria - esp
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
PS Claim 2; Fig 38; 248pp; English.
XX
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
CC regions derived from various microorganisms. These sequences were
CC used in the method of the invention for the detection and identification
CC of at least one or more microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes
CC given in AAT34011-77 to the amplified sequence. These probes were
CC specifically used to detect microorganisms in samples originating from
CC the respiratory tract. This spacer region is derived from Pseudomonas
CC stutzeri LMG 2333.
XX
SQ Sequence 504 BP; 119 A; 111 C; 137 G; 137 T; 0 other;

Query Match 53.2%; Score 265.4; DB 17; Length 504;
Best Local Similarity 78.5%; Pred. No. 2.2e-79;
Matches 412; Conservative 0; Mismatches 66; Indels 47; Gaps 6;

Qy 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAATTCGTTGATTCACCTTGCAGAAA 60
Dy 1 ATCGAAGACACCGGCTTCGTCATAAGTCCACACGAATTCGTTGATTCACCTTGCAGAAA 60
Qy 61 GCGATTGGGTTAGACCCGAGAGTACGAGTGGTCTGTAGCTCAGTGTGTTAGAGCGCA 120
Dy 61 GCGATTGGGTTAGACCCGAGAGTACGAGTGGTCTGTAGCTCAGTGTGTTAGAGCGCA 120
Qy 121 CCCCTGATAGGGTGGAGTGGCGATTCGAAATCTGCCACACCCACCAATTCGCGGATG 180
Dy 121 CCCCTGATAGGGTGGAGTGGCGATTCGAAATCTGCCACACCCACCAATTCGCGGATG 180
Qy 181 GCCAGTGTCAATGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGT 240
Dy 173 -----AAGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGAGGAGGT 221
Qy 241 CAGGAGTTCGATTCCTTGGCTCCACCACTCACTCAGATCGTGAAGACTCAGAAATG 300
Dy 222 CAGCGGTTTCGATTCCTGCTCCACCACTCACTCAGATCGTGAAGACTCAGAAATG 280
Qy 301 AACATT-----GGTAGTTCATGTTGATTTCTGCTCTTTCGCGCC 339

Db 281 AGTGTTCACAGGATGAGTTGATTCGCTGGTTGAACATGATTTCTGGACTTTCGCC 340
Qy 340 AGAAGTGTCTTTAAAAATTTGGGTATGTGATAGAGTGAACACAGG-----TGTTC 395
Db 341 AGAAGTGTCTTTAAAAATTTGGGTATGTGATAGAGTGAACACAGGATGTGTGCTTTC 400
Qy 396 CTGCACGTTGTTAATCAAGCAAAATTTGCCAGTTC-AAGCGCGAATTTTCGGCGAATGT 454
Db 401 GGCAGATGTCGCTCAAGGTAAATTTGCGTGTCTCTATGCAATTTTCGGCGAATGT 460
Qy 455 CGTCTTCACGTTAGCAATCTATAACACGATTCGTTGGGGTTATAT 499
Db 461 CGTCTTCAGTTA-TAGACAGTAAACAGATTGCTTGGGGTTATAT 504

RESULT 4
AAT11846
ID AAT11846 standard; DNA; 468 BP.
XX
AC AAT11846;
XX
DT 03-SEP-1996 (first entry)
XX
DE P. putida LMG 2232 16S-23S rRNA spacer region.
XX
KW Probe; detection; identification; microorganism; amplify;
KW 16S-23S rRNA spacer region; respiratory tract; universal;
KW species-specific; ss.
XX
OS Pseudomonas putida.
XX
PN WO9600298-Al.
XX
PD 04-JAN-1996.
XX
PF 23-JUN-1995; 95WO-EP02452.
XX
PR 07-APR-1995; 95EP-0870032.
XX
PR 24-JUN-1994; 94EP-0870106.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Jannes G, Rossau R, Van Heuverswyn H;
XX
DR WPI; 1996-068882/07.
XX
PT Novel hybridisation assay for the detection of eubacteria - esp
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
PS Claim 2; Fig 40; 248pp; English.
XX
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
CC regions derived from various microorganisms. These sequences were
CC used in the method of the invention for the detection and identification
CC of at least one or more microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes
CC given in AAT34011-77 to the amplified sequence. These probes were
CC specifically used to detect microorganisms in samples originating from
CC the respiratory tract. This spacer region is derived from Pseudomonas
CC putida LMG 2232.
XX
SQ Sequence 468 BP; 117 A; 101 C; 117 G; 133 T; 0 other;

Query Match 39.8%; Score 198.4; DB 17; Length 468;
Best Local Similarity 72.8%; Pred. No. 1e-56;
Matches 367; Conservative 0; Mismatches 96; Indels 41; Gaps 7;

Qy 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAATTCGTTGATTCACCTTGCAGAAA 60
Dy 1 ATCGACGACATCATCGTGTCTCTAAGTCCACACGAATTCGTTGATTCATGAGAGA 60
Qy 61 GCGATTGGGTTAGACCCGAGAGTACGAGTGGTCTGTAGCTCAGTGTGTTAGAGCGCA 120

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Db 61 CGATTAGTTAGCAACCTT-----CGATTGGTCTGTAGCTAGTTGGTTAGAGCGCA 113  
 QY 121 CCCCTGATAAGGGTGAGTTCGGCAGTTCCGAATCTGCCAGACCCACCAATTTGTCGGGATG 180  
 Db 114 CCCCTGATAAGGGTGAGTTCGGCAGTTCCGAATCTGCCAGACCCACCAATTTGC----- 167  
 QY 181 GCCAGTGTCAAAATGGGGCCATAGCTAGCTGGGAGAGCGCTGCTTTGCAGCGCAGGAGGT 240  
 Db 168 -----TGGGGCCATAGCTAGCTGGGAGAGCGCTGCTTTGCAGCGCAGGAGGT 215  
 QY 241 CAGGAGTTCGATCTCTTGGCTCCACCA--TCAACTCAGATCGCTGAAAGCTCAGAAA 298  
 Db 216 CAGGGTTCGATCCGCTTGCTCCACACCCCGCTTGCAGAGTTGTCAAAAGCTTAGAAA 275  
 QY 299 TGAACATTTGGTGTAGTCAATGTGATTCTGCTCTTTGGCGCAGCACTGTTCTTTAAAAAT 358  
 Db 276 TGAATATTCG-CGTCGAATATGATTTCTGACCTTT--ATCAGAACTCGTCTCTTTAAAAAT 332  
 QY 359 TTGGGTATGTGATAGA---AGTGACTAACAGCGGTGTTTCACTGCACCGTTGTTAATCAAGG 415  
 Db 333 TTGGGTATGTGATAGAAGATAGACTGGACAGCACTTTCACCTGCTGTGTTCAGGCTAA 392  
 QY 416 CAAAATTTGGCAGTTCAAGCGCAATTTTCGGCGAATGCTGCTCTTACGTTTACGAATCTA 475  
 Db 393 GGTAAATTTGTGAGTAATTACAAAGTTTTCGGCGAATGTTGTCTTCAC-----AGTA 444  
 QY 476 TAACCAAGATTCCTTGGGGTTATAT 499  
 Db 445 TAACCAAGATTCCTTGGGGTTATAT 468

## RESULT 5

AAT11843

ID AAT11843 standard; DNA; 520 BP.

XX

AC AAT11843;

XX

DT 03-SEP-1996 (first entry)

XX

DE P. psedocaligenes IMG 1225 16S-23S rRNA spacer region.

XX Probe; detection; identification; microorganism; amplify;

KW 16S-23S rRNA spacer region; respiratory tract; universal;

KW species-specific; ss.

XX

OS Pseudomonas pseudoalcaligenes.

XX

PN WO9600298-A1.

XX

PD 04-JAN-1996.

XX

PF 23-JUN-1995; 95WO-EP02452.

XX

PR 07-APR-1995; 95EP-0870032.

XX

PR 24-JUN-1994; 94EP-0870106.

XX

PA (INNO-) INNOGENETICS NV.

XX

PI Jannes G, Rossau R, Van Heuverswyn H;

XX

DR WPI; 1996-068882/07.

XX

PT Novel hybridisation assay for the detection of eubacteria - esp

PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region

XX

PS Claim 2; Fig 37; 248pp; English.

XX

CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer

CC regions derived from various microorganisms. These sequences were

CC used in the method of the invention for the detection and identification

CC of at least one or more microorganisms. The method comprises amplifying

CC the 16S-23S rRNA spacer region and hybridising one or more of the probes

CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from Pseudomonas  
 CC pseudoalcaligenes IMG 1225.

SQ Sequence 520 BP; 126 A; 109 C; 134 G; 151 T; 0 other;

Query Match 38.7%; Score 193.2; DB 17; Length 520;  
 Best Local Similarity 72.8%; Pred. No. 6.4e-55;  
 Matches 386; Conservative 0; Mismatches 103; Indels 41; Gaps 9;

QY 1 ATCGAAGCACTTTCAGCTTCTTCATAAGTTCCACACAGAAATTCCTGATTCACCTTTCGCAAAA 60

Db 1 ATCGAAGCACTTCAGCTTCTTCATAAGTTCCACACAGAAATTCCTGATTCACCTTTCGCAAAA 60

QY 61 GCGATTGGTGTGACACCGGAGAGTGCAGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120

Db 61 AATGCTGTAAAGCGGACCGCTGTATA-----GGTCTGTAGCTCAGTTGGTTAGAGCGCA 114

QY 121 CCCCTGATAAGGGTGAGTTCGGCAGTTCCGAATCTGCCAGACCCACCAATTTGTCGGGATG 180

Db 115 CCCCTGATAAGGGTGAGTTCGGCAGTTCCGAATCTGCCAGACCCACCAATTTGTCGGGATG 171

QY 181 GCCAGTGTCAAAATGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTTGCAGCGAGGAGGT 240

Db 172 TCGAGAGAAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCAGCGAGGAGGT 231

QY 241 CAGGAGTTCGATCTCTTGGCTCCACCATCACTCAG-----ATCGCTGAAAGC 291

Db 232 CAGGGTTCGATCCCGCTTGGCTCCACCATCTCTCTGTTGCGGTGAGTGTAAAGAGT 291

QY 292 TCAGAAATGA-----ACATTGGTAGTTCAATGTTGATTCTTCTGCTTT----- 334

Db 292 TCAGAAATGATGCGGCTTCAGTTTCTGCTTTCAGTGTCTGATTTCTGCTTTTGACCG 351

QY 335 GCGCCAGAACTGTTCTTTTAAAAATTTGGGTATGTGATAGTAGAGTCACTAACAGCGCTG-TTT 393

Db 352 GTACGAAATCGTCTTTTAAAAATTTGGGTATGTGATAGTAGAGTCACTAACAGCGCTG-TTT 411

QY 394 CACTGCACTGTG--TTAATCAAGGCAAAATTTG--CGAGTTCAAGCGGAAATTTTCGCG 449

Db 412 CACTGCAATGTATGCTGCTCAAGTAAATTTGTAGTTCACAGACCAATTTTCGCG 471

QY 450 AATGTCGTCTTCAGTTTACAAATCTATPACCAAGATTCCTTTGGGTTATAT 499

Db 472 AATGTCGTCTTCAGTAT--TGAGACAGTAACCAAGATTCCTTTGGGTTATAT 520

## RESULT 6

AAI69774

ID AAI69774 standard; DNA; 588 BP.

XX

AC AAI69774;

XX

DT 13-DEC-2001 (first entry)

XX

DE 16S/23S rRNA spacer region.

XX

KW Bacterium detection; 16S/23S rRNA spacer region; ds.

XX

OS Pseudomonas putida.

XX

PN JP2001190279-A.

XX

PD 17-JUL-2001.

XX

PF 13-JAN-2000; 2000JP-0004160.

XX

PR 13-JAN-2000; 2000JP-0004160.

XX

PA (MITO) MITSUBISHI JUKOGYO KK.

XX

DR WPI; 2001-605311/69.

XX PT Detection method of Pseudomonas bacteria -  
XX PS Claim 6; Page 7; 11pp; Japanese.  
XX CC The present invention relates to a method for the detection of the  
CC present DNA sequence: the 16S/23S rRNA spacer region of Pseudomonas  
CC putida. The method can be used to detect Pseudomonas bacteria.  
XX SQ Sequence 588 BP; 147 A; 134 C; 153 G; 149 T; 5 other;  
Query Match 31.8%; Score 158.6; DB 22; Length 588;  
Best Local Similarity 71.5%; Pred. No. 3.6e-43;  
Matches 369; Conservative 0; Mismatches 84; Indels 63; Gaps 10;  
QY 1 ATCGAAGACTTCAGCTTCTTCATAGTCCACAGCAATGCTGATTCACTTGGCAAAA 60  
DB 63 ATCGAGCATCAGCTGCTGATGAGTCCACACAGCAATGCTGATTCACTTGGCAAGA 122  
QY 61 GCGATTGGGTGAGACCCGAGAGTGACGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA 120  
DB 123 C-----GATCAAGACCCCTATA-----TAGGCTGTGTAGCTCAGTTGGTTAGAGCGCA 168  
QY 121 CCCTGATAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTCGGGATG 180  
DB 169 CCCTGATAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTCGGGATG 218  
QY 181 GCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCCCTGCTTTGACGACGAGAGT 240  
DB 219 -----ATGGGGGCCATAGCTCAGCTGGGAGAGCCCTGCTTTGACGACGAGAGT 269  
QY 241 CAGGAGTTCGATCTCTTGGCTCCACATCACTCAGCTCAGTCAAGAGCTCAGAAATG 300  
DB 270 CAGCGGATCGATCCCGCTTGGCTCCACATCACTCAGCTCAGTCAAGAGCTCAGAAATG 328  
QY 301 AACATTGGTATGATGATGTTCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
DB 329 AGCAT--CCGCTATATGATGTTCTGCTTGTG--TCAGATCGCTTCTTAAATTC 384  
QY 361 GGGTATGTATAGA-AGTGAATCAAGCGGTGTTTCACTGACGCTTGTAA--TCAGGCA 417  
DB 385 GGATATGTATAGATATAGACTGAACACCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 444  
QY 418 AATTTCGAGTTC-----RAGCGCAATTTTCGCGCAATTTGCTGCTTTCAC 463  
DB 445 AATTTCGAGTTC-----RAGCGCAATTTTCGCGCAATTTGCTGCTTTCAC 504  
QY 464 GTTACGAATCTATAACCAAGATGCTGGGTTATAT 499  
DB 505 -----AGTATAACCAAGATGCTGGGTTATAT 532  
RESULT 7  
AAH54998/c  
ID AAT11898 standard; DNA; 470 BP.  
XX AC AAT11898;  
XX DT 03-SEP-1996 (first entry)  
XX DE Yersinia enterocolitica strain p95 16S-23S rRNA spacer region (#1).  
XX KW Probe; detection; identification; microorganism; amplify;  
XX KW 16S-23S rRNA spacer region; food; universal;  
XX KW species-specific; ss.  
XX OS Yersinia enterocolitica.  
XX PN WO9600298-A1.  
XX PD 04-JAN-1996.  
XX PF 23-JUN-1995; 95WO-EP02452.  
XX PT Detection method of Pseudomonas bacteria -  
XX PS Claim 6; Page 7; 11pp; Japanese.  
XX CC The present invention relates to a method for the detection of the  
CC present DNA sequence: the 16S/23S rRNA spacer region of Pseudomonas  
CC putida. The method can be used to detect Pseudomonas bacteria.  
XX SQ Sequence 588 BP; 147 A; 134 C; 153 G; 149 T; 5 other;  
Query Match 31.8%; Score 158.6; DB 22; Length 588;  
Best Local Similarity 71.5%; Pred. No. 3.6e-43;  
Matches 369; Conservative 0; Mismatches 84; Indels 63; Gaps 10;  
QY 1 ATCGAAGACTTCAGCTTCTTCATAGTCCACAGCAATGCTGATTCACTTGGCAAAA 60  
DB 63 ATCGAGCATCAGCTGCTGATGAGTCCACACAGCAATGCTGATTCACTTGGCAAGA 122  
QY 61 GCGATTGGGTGAGACCCGAGAGTGACGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA 120  
DB 123 C-----GATCAAGACCCCTATA-----TAGGCTGTGTAGCTCAGTTGGTTAGAGCGCA 168  
QY 121 CCCTGATAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTCGGGATG 180  
DB 169 CCCTGATAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGTCGGGATG 218  
QY 181 GCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCCCTGCTTTGACGACGAGAGT 240  
DB 219 -----ATGGGGGCCATAGCTCAGCTGGGAGAGCCCTGCTTTGACGACGAGAGT 269  
QY 241 CAGGAGTTCGATCTCTTGGCTCCACATCACTCAGCTCAGTCAAGAGCTCAGAAATG 300  
DB 270 CAGCGGATCGATCCCGCTTGGCTCCACATCACTCAGCTCAGTCAAGAGCTCAGAAATG 328  
QY 301 AACATTGGTATGATGATGTTCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
DB 329 AGCAT--CCGCTATATGATGTTCTGCTTGTG--TCAGATCGCTTCTTAAATTC 384  
QY 361 GGGTATGTATAGA-AGTGAATCAAGCGGTGTTTCACTGACGCTTGTAA--TCAGGCA 417  
DB 385 GGATATGTATAGATATAGACTGAACACCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 444  
QY 418 AATTTCGAGTTC-----RAGCGCAATTTTCGCGCAATTTGCTGCTTTCAC 463  
DB 445 AATTTCGAGTTC-----RAGCGCAATTTTCGCGCAATTTGCTGCTTTCAC 504  
QY 464 GTTACGAATCTATAACCAAGATGCTGGGTTATAT 499  
DB 505 -----AGTATAACCAAGATGCTGGGTTATAT 532  
RESULT 8  
AAH54998/c  
ID AAT11898 standard; DNA; 2839 BP.  
XX AC AAT11898;  
XX DT 03-SEP-2001 (first entry)  
XX DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4362.  
XX KW Staphylococcus epidermidis SR1 strain; infection; diagnosis;  
XX KW vaccination; endocarditis; ds.  
XX OS Staphylococcus epidermidis.  
XX PN WO200134809-A2.  
XX PD 17-MAY-2001.  
XX PF 09-NOV-2000; 2000WO-US30782.  
XX PR 09-NOV-1999; 99US-0164258.  
XX PA (GLAXO) GLAXO GROUP LTD.  
XX PI Kimmerly WJ;







DT 16-MAR-1999 (first entry)  
 DE Staphylococcus aureus contig SEQ ID #3711.  
 XX Computer readable medium; vaccine; S.aureus infection; immunodetection;  
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
 KW skin infection; surgical wound infection; scalded skin syndrome;  
 KW toxic shock syndrome; ds.  
 XX Staphylococcus aureus.  
 OS EP786519-A2.  
 XX 30-JUL-1997.  
 PD 07-JAN-1997; 97EP-0100117.  
 XX 05-JAN-1996; 96US-0009861.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;  
 PI Rosen CA;  
 XX WPI; 1997-374922/35.  
 DR Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
 PT stored on computer readable medium and used in the production of  
 PT anti-S.aureus vaccines  
 XX Claim 1; Page 2654; 3271pp; English.  
 XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
 CC of the invention. The DNA sequences are recorded on a computer readable  
 CC medium, preferably selected from a floppy or hard disk, random access  
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
 CC the S.aureus DNA sequences allows putative functions to be assigned so  
 CC that protein-encoding or regulatory regions of commercial, therapeutic or  
 CC industrial importance can be obtained. Specifically, sequences which are  
 CC likely to encode antigens have been identified and these polypeptides can  
 CC be used in a vaccine composition against S.aureus infection. The  
 CC polypeptides can also be used in a kit for the immunodetection of  
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
 CC for recombinant production of the polypeptides. The new DNA sequences  
 CC (and their fragments) are useful as primers or probes for isolating  
 CC homologues of any of the S.aureus DNA sequences contained on the  
 CC computer readable medium.  
 XX Sequence 400 BP; 104 A; 79 C; 104 G; 113 T; 0 other;  
 SQ Query Match 20.5%; Score 102.4; DB 18; Length 400;  
 Best Local Similarity 76.6%; Pred. No. 3.2e-24;  
 Matches 141; Conservative 0; Mismatches 36; Indels 7; Gaps 1;  
 QY 89 ATTGGGTCTGCTAGCTAGTGGTTAGAGCCACCCCTGATAGAGGTGAGTGGCAGTTC 148  
 Db 187 AATGGCCCTATAGCTAGTGGTTAGAGCCACCCCTGATAGAGGTGAGTGGTTC 246  
 QY 149 GAATCTGCCAGACCCACCAATGTCTGGGATGCGGATGCAATGGGCCATAGCTCAG 208  
 Db 247 GAGTCCACTTAGGCCACCATTT-----AATTATACCTAATTTGGGGCTTAGCTCAG 299  
 QY 209 CTGGGAGAGGCGCTGTTTGCAGCAGGAGGTGAGTGGATCTGCTTGGCTCCACC 268  
 Db 300 CTGGGAGAGCGCGCTGTTTGCAGCAGGAGGTGAGTGGATCTGCTTGGCTCCACC 359  
 QY 269 ATCA 272  
 Db 360 ATTA 363

RESULT 13  
 AAV77902/c  
 ID AAV77902 standard; DNA; 400 BP.  
 XX AAV77902;  
 AC AAV77902;  
 XX 16-MAR-1999 (first entry)  
 DT Staphylococcus aureus contig SEQ ID #3591.  
 XX Computer readable medium; vaccine; S.aureus infection; immunodetection;  
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
 KW skin infection; surgical wound infection; scalded skin syndrome;  
 KW toxic shock syndrome; ds.  
 XX Staphylococcus aureus.  
 OS EP786519-A2.  
 XX 30-JUL-1997.  
 PD 07-JAN-1997; 97EP-0100117.  
 XX 05-JAN-1996; 96US-0009861.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;  
 PI Rosen CA;  
 XX WPI; 1997-374922/35.  
 DR Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
 PT stored on computer readable medium and used in the production of  
 PT anti-S.aureus vaccines  
 XX Claim 1; Page 2600; 3271pp; English.  
 XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
 CC of the invention. The DNA sequences are recorded on a computer readable  
 CC medium, preferably selected from a floppy or hard disk, random access  
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
 CC the S.aureus DNA sequences allows putative functions to be assigned so  
 CC that protein-encoding or regulatory regions of commercial, therapeutic or  
 CC industrial importance can be obtained. Specifically, sequences which are  
 CC likely to encode antigens have been identified and these polypeptides can  
 CC be used in a vaccine composition against S.aureus infection. The  
 CC polypeptides can also be used in a kit for the immunodetection of  
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
 CC for recombinant production of the polypeptides. The new DNA sequences  
 CC (and their fragments) are useful as primers or probes for isolating  
 CC homologues of any of the S.aureus DNA sequences contained on the  
 CC computer readable medium.  
 XX Sequence 400 BP; 105 A; 82 C; 66 G; 107 T; 40 other;  
 SQ Query Match 20.5%; Score 102.4; DB 18; Length 400;  
 Best Local Similarity 76.6%; Pred. No. 3.2e-24;  
 Matches 141; Conservative 0; Mismatches 36; Indels 7; Gaps 1;

QY 89 ATTGGGTCTGCTAGCTAGTGGTTAGAGCCACCCCTGATAGAGGTGAGTGGCAGTTC 148

Db	276	AATGGGCCTATAGCTACGCTGGTGTAGAGCGCACGCCCTGATAAGCGTGAGTTCGGTGGTTC	217
QY	149	GAATCTGCCAGACCCACCAATTCGCGGATGGCCAGTGTCAAATGGGGCCATAGCTCAG	208
Db	216	GAGTCACACTTAGGCCACCACTT-----AATTTAATACCTATTTGGGGGCTTAGCTCAG	164
QY	209	CTGGGAGAGCGCCTGCTTTGCACGCAGAGGTTCAGGAGTTCGATCCTCCTTTGGGTCACC	268
Db	163	CTGGGAGAGCGCCTGCTTTGCACGCAGAGGTTCAGCGGTTCCGATCCCGCTAGTCTCCACC	104
QY	269	ATCA 272	
Db	103	ATTA 100	
RESULT 14			
AAV77852	ID	AAV77852 standard; DNA; 1311 BP.	
XX	AC	AAV77852;	
XX	XX		
DE	16-MAR-1999	(first entry)	
XX	XX	Staphylococcus aureus contig SEQ ID #3541.	
XX	XX		
KW	Computer readable medium; vaccine; S.aureus infection; immunodetection;		
KW	cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;		
KW	skin infection; surgical wound infection; scalded skin syndrome;		
KW	toxic shock syndrome; ds.		
XX	XX		
OS	Staphylococcus aureus.		
XX	XX		
PN	EP786519-A2.		
XX	XX		
PD	30-JUL-1997.		
XX	XX		
PF	07-JAN-1997; 97EP-0100117.		
XX	XX		
PR	05-JAN-1996; 96US-0009861.		
XX	XX		
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX	XX		
PI	Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;		
PI	Rosen CA;		
XX	XX		
DR	WPI; 1997-374922/35.		
XX	XX		
PT	Polynucleotide(s) and proteins derived from Staphylococcus aureus -		
PT	stored on computer readable medium and used in the production of		
PT	anti-S.aureus vaccines		
XX	XX		
PS	Claim 1; Page 2576; 3271pp; English.		
XX	XX		
CC	This sequence represents one of 5191 Staphylococcus aureus DNA sequences		
CC	of the invention. the DNA sequences are recorded on a computer readable		
CC	medium, preferably selected from a floppy or hard disk, random access		
CC	memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using		
CC	the S.aureus DNA sequences allows putative functions to be assigned so		
CC	that protein-encoding or regulatory regions of commercial, therapeutic or		
CC	industrial importance can be obtained. Specifically, sequences which are		
CC	likely to encode antigens have been identified and these polypeptides can		
CC	be used in a vaccine composition against S.aureus infection. The		
CC	polypeptides can also be used in a kit for the immunodetection of		
CC	S.aureus in a sample. S.aureus is implicated in numerous human diseases,		
CC	including cellulitis, eyelid infections, food poisoning, osteomyelitis,		
CC	skin and surgical wound infections, scalded skin syndrome, toxic shock		
CC	syndrome, etc. Organisms transformed with the DNA sequences can be used		
CC	for recombinant production of the polypeptides. The new DNA sequences		
CC	(and their fragments) are useful as primers or probes for isolating		
CC	homologues of any of the S.aureus DNA sequences contained on the		
CC	computer readable medium.		
XX	XX		

CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
CC for recombinant production of the polypeptides. The new DNA sequences  
CC (and their fragments) are useful as primers or probes for isolating  
CC homologues of any of the *S. aureus* DNA sequences contained on the  
CC computer readable medium.

SQ Sequence 400 BP; 115 A; 95 C; 78 G; 109 T; 3 other;

Query Match 20.0%; Score 99.8; DB 18; Length 400;

Best Local Similarity 75.5%; Pred. No. 2.5e-23;

Matches	139;	Conservative	0;	Mismatches	38;	Indels	7;	Gaps	1;
---------	------	--------------	----	------------	-----	--------	----	------	----

Qy 89 ATTGGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGATAAGGTTGAGGTGGCAGTTC 148

Db 272 AATGGGCGCTATAGCTCAGCTGGTTAGAGCGCACGCCCTGATAAGCGTGAGGTCCGGTGGTTC 213

QY 149 GAATCTGCCCAGACCCACCAATTGTCGGGATGGCCAGTGTCAAATGGGCCATAGCTCAG 208

212	GAGTCCACCTTAGGCCCCCCCCATT-----AATTATAATACCTNTTTGGGGGGTTAGCTCAG	160
Db		

QY 209 CTGGAGAGCGCCTGCTTTGCACGAGGAGTTCGATCCTCCTTGGCTCCACC 268

Db 159 CTGGGAGAGCGCCTGCTTTGCACGCACGAGGTCAGCGGTTTCGATCCCGCTAGTCTCCACC 100

QY 269 ATCA 272

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—  
—

Search completed: February 1, 2003, 01:37:30  
Job time : 127.163 secs

•





Patent No. 6025132  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
TITLE OF INVENTION: HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 471 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-111

Query Match	54.6%	Score 272.6;	DB 3;	Length 471;
Best Local Similarity	80.7%;	Pred. No. 6.1e-86;		
Matches 409; Conservative	0;	Mismatches 54;	Indels 44;	Gaps
QY 1	ATCGAAGACTTCAGCTCTTTCATAAGTCCACACAGAATGCTTGATTCAGTTCGCGAAA	60		
DB 1	ATCGAAGATCCCGGCTCTTCATAAGTCCACACAGANTGCTTGATTCAGTCTGTTA	57		
QY 61	GCATTTGGGTTGACACCGAGAGTGACGATGGGTCGTAGCTCAGTTGGTTAGAGCGCA	120		
DB 58	-----GACGATGGGTCGTAGCTCAGTTGGTTAGAGCGCA	93		
QY 121	CCCTGATAAGGGTAGGTCGGCAGTTCGAAATCTGCCACAGCCACCAATTTGTCGGGATG	180		
DB 94	CCCTGATAAGGGTAGGTCGGCAGTTCGAAATCTGCCAGACCCACCAATTTGTCGTG	153		
QY 181	GCCAGT---TCAAAATGGGGCCATAGCTCAGCTGGAGAGCGCTGCTTGACGCGAGA	237		
DB 154	CTGCGTATCCGATACGGGGCCATAGCTCAGTGGAGAGCGCGCTGCTTGACGCGAGA	213		
QY 238	GGTCAGGAGTTCGATCCCTCTTGGGTCACCATCACTCAGATCGCTGAAAGCTCAGAA	297		

Db	214	GGTCAGGAGTTCGATCCCTCCCTGGCTCCACCATCTA-AAACAATCGTGAAGCTCAGAA	272
Qy	298	ATGAACAATGGTAGTTCAATGTTGATTTCTGGTCTTTGGCCGAGAACATGTTCTTTAAAAA	357
Db	273	ATGAATGTTCTGGTAGTAACATGATTTCTGGTCTTTGCGCCGAGAACATGTTCTTTAAAAA	332
Qy	358	TTTGGGTATGTATAGAAAGTGA--CTAACAGCGTGGTTTCTCACTGCACGTTCTT--AATCA	412
Db	333	TTCCGGTATGTATAGAAAGTGAAGTGAATGATCTCTTTCACTGGTGATCATTCGAAGTCA	392
Qy	413	AGGCAAAATTTGCGAGTTTCAAGCGCGAAATTTTCGGCGAATTCGTCTTTCACGTTACGAAT	472
Db	393	AGGTAATAATTTGCGAGTTTCAAGCGCGAAATTTTCGGCGAATTCGTCTTTCACGTTACGAAT	472
Qy	473	CTATAACCAAGATTGCTTGGGGTTATAT	499
Db	445	GTAATAACCAAGATTGCTTGGGGTTATAT	471
RESULT 4			
US-09-448-894-111			
; Sequence 111, Application US/09448894			
; Patent No. 6312903			
; GENERAL INFORMATION:			
; APPLICANT: JANNES, GEERT			
; ROSSAU, RUDI			
; VAN HEUVERSWYN, HUGO			
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION			
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A			
; HYBRIDIZATION ASSAY			
; NUMBER OF SEQUENCES: 216			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: NIXON & VANDERHUYE P.C.			
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR			
; CITY: WASHINGTON			
; STATE: D.C.			
; COUNTRY: USA			
; ZIP: 22201			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/448,894			
; FILING DATE: 29-No. 6312903-1999			
; CLASSIFICATION: <Unknown>			
; 07-APR-1995			
; 24-JUN-1994			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/765,332			
; FILING DATE: <Unknown>			
; APPLICATION NUMBER: EP 95870032.0			
; FILING DATE: 07-APR-1995			
; APPLICATION NUMBER: EP 94870106.5			
; FILING DATE: 24-JUN-1994			
; ATTORNEY/AGENT INFORMATION:			
; NAME: SADOFF, B.J.			
; REGISTRATION NUMBER: 36,663			
; REFERENCE/DOCKET NUMBER: 1487-14			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 703-816-4091			
; TELEFAX: 703-816-4100			
; INFORMATION FOR SEQ ID NO: 111:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 471 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: cDNA			
; HYPOTHETICAL: NO			
; ANTI-SENSE: NO			





ROSSAU, RUDI  
VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-1999  
CLASSIFICATION: <Unknown>  
07-APR-1999  
24-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 113:  
US-09-448-894-113

Query Match 53.2%; Score 265.4; DB 4; Length 504;  
Best Local Similarity 78.5%; Pred. No. 2.1e-83;  
Matches 412; Conservative 0; Mismatches 66; Indels 47; Gaps 6;

QY 1 ATCGAAGACTGACCTCTTCATAAGTTCACACAGCAATGCTGTGATCTTCTGCGGAAA 60  
|||||  
DB 1 ATCGAAGACACCGGCTTCGTCATAAGTTCACACAGCAATGCTGTGATCTTCTGCGGAAA 60  
|||||

QY 61 GCGATTGGTGTAGACCCGAGAGTACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
|||||  
DB 61 GCGATTGGTGTAGACCCGAGAGTACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
|||||

QY 121 CCCTGTATAAGGTGAGGTGCGGAGTTCGAATCTGCCACACCCACCAATGTCGGGATG 180  
|||||  
DB 121 CCCTGTATAAGGTGAGGTGCGGAGTTCGAATCTGCCACACCCACCAATGTCGGGATG 180  
|||||

QY 181 GCGAGTCTCAAAATGGGCCATAGCTCAGCTGGGAGCGCTGCTTTGCGAGGAGGT 240  
|||||  
DB 173 -----AGGGGCCATAGCTCAGCTGGGAGCGCTGCTTTGCGAGGAGGT 221  
|||||

QY 241 CAGGAGTTCGATCCTCTGGCTCCACCATCACTACGATCGCTGAAAGCTCAGAAATG 300  
|||||  
DB 222 CAGGGTTTCGATCCGCTTGGCTCCACCATTAACCTAG-TCGCGGAAAGCTCAGAAATG 280  
|||||

QY 301 AACATT-----GGTAGTTCAATGTTGATTCTCTGCTTTGCGCC 339  
|||||  
DB 281 AGTGTTCACAGAGTAGGTTGATTGCTGGTGTGAACATTGATTCGAGCTTTGCGCC 340  
|||||

QY 340 AGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAAGTGACTAACACAGCG----TGTTTCA 395  
|||||  
DB 341 AGAACTGTTCTTTAAAAATTTGGGTATGTGATAGAAGTAGACCGATGTGTTGCTTTCACT 400  
|||||

QY 396 CTGCACGTTGTTAATCAAGCAAAATTTGCGAGTTC-AAGCGGGAATTTTCGGCGAATGT 454  
|||||  
DB 401 GGCAGCATGTGCGCTCAAGGTAAATTTGCGTGTCTCTATGCAAAATTTTCGGCGAATGT 460  
|||||

QY 455 CGTCTTCACGTTACGAATCTATAACCAAGATTGCTTGGGGTTATAT 499  
|||||  
DB 461 CGTCTTCACGTTA-TAGACAGTAACCAAGATTGCTTGGGGTTATAT 504  
|||||

## RESULT 7

US-08-765-332-115  
; Sequence 115, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-765-332-115



;; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
;; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
;; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
;; NUMBER OF SEQUENCES: 216  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: NIXON & VANDERHYE P.C.  
;; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
;; CITY: WASHINGTON  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 22201  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/EP95/02452  
;; FILING DATE: 23-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 95870032.0  
;; FILING DATE: 07-APR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 94870106.5  
;; FILING DATE: 24-JUN-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: SADOFF, B.J.  
;; REGISTRATION NUMBER: 36,663  
;; REFERENCE/DOCKET NUMBER: 1487-14  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-816-4091  
;; TELEFAX: 703-816-4100  
;; INFORMATION FOR SEQ ID NO: 112:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 520 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; MOLECULE TYPE: CDNA  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; US-08-765-332-112

Query Match 38.7%; Score 193.2; DB 3; Length 520;  
Best Local Similarity 72.8%; Pred. No. 4.9e-58;  
Matches 386; Conservative 0; Mismatches 103; Indels 41; Gaps 9;

QY 1 ATCGAAGACTTCAGCTTCTTCATAAGTCCACACGAATTCGTTGATTCACCTGCGAATA 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 1 ATCGAAGACATCAGCTTCTTCATAAGTATCCACACGAATTCGTTGATTCATAGTCGAACG 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 61 GCATTTGGTTGACACCCGAGAGTGACGATGGTGTGTAGCTCAGTTCAGTTGAGCGCA 120  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 61 ATGCTGTAAACGCGACCGCTGTTATA-----GGTCTGTAGCTCAGTTCAGTTGAGCGCA 114  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 121 CCCTGATAGGTTGAGTGGCGGAGTTCGAATCTGCCACGACCCACCAATTCGCGGATG 180  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 115 CCCTGATAGGTTGAGTGGCGGAGTTCGAATCTGCCACGACCCACCAATTCGCGGATG 171  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 181 GCAGTGTCAATGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGCGAGGAGT 240  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 172 TCAGAAGAATACGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTTCACGCGAGGAGT 231  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 241 CAGGAGTTCGATCCTCTTGGCTCCACATCACTCAGC-----ATCGCTGAAGC 291  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 232 CAGCGGTTCCGATCCCGCTGGCTCCACCATCTCTCTGCTGTGGGTGAGTGTAAAGAGT 291  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 292 TCAGAATGA-----ACATGGTAGTTCAATGTTGATTCGTTCTGCTTTT----- 334  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

DB 292 TCAGAATGATGCCCTTCAGCTTGTCTCTGTGAGTCTGATTCGTTCTGCTTTTGACCG 351  
QY 335 GCGCCAGAACCTGCTCTTTTAAAAATTTGGGTATGTGATGAAGTGAACAGCGTG-TTT 393  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 352 GTACGAAAATCGTCTCTTTAAAAATTTGGATATGTGATGAAGTGAATTAATTCGTTT 411  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 394 CACTGCACGTTG--TTAATCAAGGCAAAATTTG--CGAGTTCAAGCGGCAATTTTCGGCG 449  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 412 CACTGGCAATTCATCTGCTCAAGGTAAATTTGTAGTTCTCTCAAGACGCAAAATTTTCGGCG 471  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
QY 450 AATGTCGCTTCACGTTACGAATCTATAACAGAGATTGCTTGGGGTTATAT 499  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 472 AATGTCGCTTCAGGAT-TGACACAGTACACAGATTGCTTGGGGTTATAT 520  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

## RESULT 10

US-09-448-894-112  
; Sequence 112, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; VAN HEUVERSWYN, HUGO  
; ROSSAU, RUDI  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/448,894  
; FILING DATE: 29-No. 6312903-1999  
; CLASSIFICATION: <Unknown>  
; 07-APR-1995  
; 24-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/765,332  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 112:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 520 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:  
US-09-448-894-112

Query Match 38.7%; Score 193.2; DB 4; Length 520;  
Best Local Similarity 72.8%; Pred. No. 4.9e-58;

Matches 386; Conservative 0; Mismatches 103; Indels 41; Gaps 9;

QY 1 ATCGAGACTTCAGCTTCTTCAAGTCCACACGAAATGCTGATTCACATTCGGAAGA 60  
|||||  
Db 1 ATCGAAGACATCAGCTTCTTCAAGTATCCACACGAAATGCTGATTCATAGTGAACG 60  
|||||  
QY 61 GCGATTGGTTCAGACCCGAGAGTACGATTTGGTCTGTAGTCTAGTTCGTTAGAGCGCA 120  
|||||  
Db 61 AATGCTGTAAACCGACCCGCTGTATATATATATATATATATATATATATATATAT 114  
|||||  
QY 121 CCCCTGATAAGGTCAGTTCGAGTTCGAATCTGCCACAGCCCAATTCGCGGATG 180  
|||||  
Db 115 CCCCTGATAAGGTCAGTTCGAGTTCGAATCTGCCACAGCCCAATTCGCGGATG 171  
|||||  
QY 181 GCCAGTGTCAATGGGGCCATAGCTCAGCTGGGAGAGCCCTGCTTGCACGACGAGCT 240  
|||||  
Db 172 TCGAAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCCCTGCTTGCACGACGAGCT 231  
|||||  
QY 241 CAGGAGTTCGATCTCTTGGCTCCACCATCAACTCAGC-----ATCGCTGAAAGC 291  
|||||  
Db 232 CAGCGTTCGATCCCGCTTGGCTCCACCATCTCTCGTGTGGGTGAGTGTAAAGAGT 291  
|||||  
QY 292 TCAGAAATGA-----ACATTTGAGTTCATATGATTTCTGCTCTT----- 334  
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Db 292 TCAGAAATGATCGCGCTTCAGGTTTCTGCTGTGAGTGTGATTTCTGCTCTT----- 351  
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QY 335 GCGCCAGAACTGTCTTAAATTTGGTATCTGATAGTACTAAGTACGAGCTG-TTT 393  
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Db 352 GTACGAAATCGTCTTAAATTTGGATATGTAGTACTAAGTACTAATTCCTTT 411  
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QY 394 CACTGCACCTGT--TTAATCAAGGCAAAATTTG--CGAGTTCAAGCGCAATTTTCGGGG 449  
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Db 412 CACTGCAATGTATCGTTCAGTCAAGTAAATTTGATTTCTCAAGACGCAATTTTCGGGG 471  
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QY 450 AATGTCGTCTTCAGTTCAGTATATACAGATTCGTTGGGGTTATAT 499  
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Db 472 AATGTCGTCTTCAGTATATACAGATTCGTTGGGGTTATAT 520  
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RESULT 11  
US-08-765-332-195  
; Sequence 195, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWM, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 195:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 470 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-765-332-195

Query Match 21.8%; Score 108.8; DB 3; Length 470;  
Best Local Similarity 72.9%; Pred. No. 2e-28;  
Matches 159; Conservative 0; Mismatches 47; Indels 12; Gaps 1;

QY 91 TGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGCGGAGTTTCA 150  
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Db 75 TAGGCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGGTGCGGAGTTTCA 134  
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QY 151 ATCTGCCAGACCCACCAATTTGCGGATGGCCAGTGT-----CAATGGGCG 198  
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Db 135 GTCCACTACCGCTTACCACTTCTCGAAGTGGAAAGGACTGACGAGTGTATGGGGC 194  
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QY 199 CATAGCTCAGCTGGGAGCGCTGCTTTCACGACGAGGTGAGGAGTTCGATTCCTCT 258  
|||||  
Db 195 TATAGCTCAGCTGGGAGCGCTGCTTTCACGACGAGGTGAGGAGTTCGATTCCTCT 254  
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QY 259 TGCTCCACCATCAACTCAGTGTGCTGAAAGTCTAGA 296  
|||||  
Db 255 TAGCTCCACCATATAGTCTCTGATTTCAATACTTCTAGA 292  
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RESULT 12  
US-09-448-894-195  
; Sequence 195, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWM, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/448,894  
; FILING DATE: 29-NOV-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 24-JUN-1994  
; FILING DATE: 07-APR-1995

APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 195:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 470 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 195:  
US-09-448-894-195

Query Match 21.8%; Score 108.8; DB 4; Length 470;  
Best Local Similarity 72.9%; Pred. No. 2e-28;  
Matches 159; Conservative 0; Mismatches 47; Indels 12; Gaps 1;  
QY 91 TGGGTGCTAGCTAGCTGTTAGAGCGCACCCCTGATAAGGTTAGGTGCGGAGTTTCA 150  
Db 75 TAGGCTTTAGCTAGCTAGGTTAGAGCGCACCCCTGATAAGGTTAGGTGCGGTTCAA 134  
QY 151 ATGTGCCAGACCCACCAATTGCGGATGCCAGTGT-----CAATGCGGC 198  
Db 135 GTCACTCAGCGCTACCACTTCGAAAGTCTGCAAGTGGAAAGGTTGTCACGTGATGGGGC 194  
QY 199 CATAGCTCAGCTGGGAGCGCCTGCTTTGCACGAGGAGTTCAGGAGTTCGATCCCT 258  
Db 195 TATAGCTCAGCTGGGAGCGCCTGCTTGCACGAGGAGTTCAGGAGTTCGATCCGCT 254  
QY 259 TGCTCCACCATCACTCAGCTGCGTGAAGTTCAGA 296  
Db 255 TAGCTCCACCATATAGTCTCTGTATTTCAATACTTCAGA 292

RESULT 13  
US-08-765-332-215  
Sequence 215, Application US/08765332  
Patent No. 6025132  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
TITLE OF INVENTION: HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 215:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-215

Query Match 19.8%; Score 99; DB 3; Length 463;  
Best Local Similarity 66.8%; Pred. No. 5.5e-25;  
Matches 161; Conservative 0; Mismatches 70; Indels 10; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTTAGGTAGAGCGCACCCCTGATAAGGTTAGGTGCGGAGTTTCA 151  
Db 115 GGGCTTAGCTAGCTAGCTGTTAGAGCGCACCCCTGATAAGGTTAGGTGCGGTTCA 174  
QY 152 TCTGCCAGACCCACCAATTGTCGGGA-----TGGCCAGTGTCAAAATGGGCCAT 201  
Db 175 TCCACTTAGGCGCCACTTTTGAATAAACCTTTCTTTTATATGTTAATAGGGGCTT 234  
QY 202 AGCTCAGCTGGGAGAGCGCCTGCTTTGCACGAGGAGTTCAGGAGTTCGATCCCTTGG 261  
Db 235 AGCTCAGCTGGGAGAGCGCCTGCTTTGCACGAGGAGTTCAGGAGTTCGATCCCTTGG 294  
QY 262 CTCCACCATCACTCAGATCGCTGAAAGCTCAAAATGAACATTTGGTAGTTCAATGTTG 321  
Db 295 CTCACCAAGAGATAGTTGTTCTTTGAAACTAGATAAGAAAAGTTAGTGTAAAAAGACG 354  
QY 322 A 322  
Db 355 A 355

RESULT 14  
US-09-448-894-215  
Sequence 215, Application US/09448894  
Patent No. 6312903  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
APPLICANT: ROSSAU, RUDI  
APPLICANT: VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 215:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 215:

US-09-448-894-215

Query Match 19.8%; Score 99; DB 4; Length 463;  
Best Local Similarity 66.8%; Pred. No. 5.5e-25;  
Matches 161; Conservative 0; Mismatches 70; Indels 10; Gaps 1;

QY 92 GGGTCGTAGCTCAGTGGTTAGAGCGCACCCCTGATAGGGTGAGGTGCGGCGAGTTCGAA 151  
DB 115 GGGCCCTATAGCTCAGCTGGTTAGAGCGCACCCCTGATAGCGGTGAGGTGCGGTTCGAG 174  
QY 152 TGTGCCAGACCCACCAATTTGTCGGGA-----TGGCCAGTGTCAAATGGGCCAT 201  
DB 175 TCCACTTAGGCCACCTTTTGTGAATAAACCTTTCTTTTATATATGTTAATAAGGGCCCT 234  
QY 202 AGCTCAGCTGGGAGAGCGCTGCTTTGACGAGGAGGTGAGGTGCGATCCTCCTTGG 261  
DB 235 AGCTCAGCTGGGAGAGCGCTGCTTTGACGAGGAGGTGAGGTGCGATCCTCCTTGG 294  
QY 262 CTCACCATCACTCAGATCGCTGAAGCTCAGAAATCAAGATGAGTTCATGTTG 321  
DB 295 CTCACCAAGATAGTTTCTTTGAAAACTAGATAAGAAAGTAGTGTAAAAAGAGCG 354  
QY 322 A 322  
DB 355 A 355

RESULT 15  
US-08-765-332-214  
; Sequence 214, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216

CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHUYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 214:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 475 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-214

Query Match 19.8%; Score 99; DB 3; Length 475;  
Best Local Similarity 66.8%; Pred. No. 5.6e-25;

Matches 161; Conservative 0; Mismatches 70; Indels 10; Gaps 1;

QY 92 GGGTCGTAGCTCAGTGGTTAGAGCGCACCCCTGATAGGGTGAGGTGCGGCGAGTTCGAA 151  
DB 115 GGGCCCTATAGCTCAGCTGGTTAGAGCGCACCCCTGATAGCGGTGAGGTGCGGTTCGAG 174  
QY 152 TGTGCCAGACCCACCAATTTGTCGGGA-----TGGCCAGTGTCAAATGGGCCAT 201  
DB 175 TCCACTTAGGCCACCTTTTGTGAATAAACCTTTCTTTTATATGTTAATAAGGGCCCT 234  
QY 202 AGCTCAGCTGGGAGAGCGCTGCTTTGACGAGGAGGTGAGGTGCGATCCTCCTTGG 261  
DB 235 AGCTCAGCTGGGAGAGCGCTGCTTTGACGAGGAGGTGAGGTGCGATCCTCCTTGG 294  
QY 262 CTCACCATCACTCAGATCGCTGAAGCTCAGAAATCAAGATGAGTTCATGTTG 321  
DB 295 CTCACCAAGATAGTTTCTTTGAAAACTAGATAAGAAAGTAGTGTAAAAAGAGCG 354  
QY 322 A 322  
DB 355 A 355

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Job time : 27.9431 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 03:05:22 ; Search time 27.7673 Seconds  
(without alignments)  
8073.649 Million cell updates/sec

Title: US-09-931-486-114  
Perfect score: 499  
Sequence: 1 ATCGAAGACTTCAGCTTCTT.....CAGATTGCTGGGTATAT 499

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications, NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	98.8	19.8	640681	US-09-790-988-1	Sequence 1, Appli
2	97.2	19.5	582	US-09-863-086-87	Sequence 87, Appl
3	97.2	19.5	590	US-09-863-086-88	Sequence 88, Appl
c 4	92	18.4	243	US-09-815-242-1358	Sequence 1358, Ap
c 5	91.4	18.3	255	US-09-815-242-1377	Sequence 1377, Ap
c 6	91.4	18.3	255	US-09-815-242-1402	Sequence 1402, Ap
c 7	91.4	18.3	255	US-09-815-242-1415	Sequence 1415, Ap
c 8	91.4	18.3	255	US-09-815-242-1423	Sequence 1423, Ap
c 9	91.4	18.3	255	US-09-815-242-1431	Sequence 1431, Ap
c 10	91.4	18.3	255	US-09-815-242-1454	Sequence 1454, Ap
c 11	91.4	18.3	255	US-09-815-242-1459	Sequence 1459, Ap
c 12	91.4	18.3	255	US-09-815-242-1473	Sequence 1473, Ap
c 13	91.4	18.3	255	US-09-815-242-1475	Sequence 1475, Ap
c 14	91.4	18.3	255	US-09-815-242-1544	Sequence 1544, Ap
c 15	91.4	18.3	255	US-09-815-242-1638	Sequence 1638, Ap
16	87	17.4	549	US-09-863-086-92	Sequence 92, Appl
17	87	17.4	603	US-09-863-086-85	Sequence 85, Appl
18	87	17.4	603	US-09-863-086-86	Sequence 86, Appl
19	87	17.4	3309400	US-09-738-626-1	Sequence 1, Appli

20	84.6	17.0	498	10	US-09-863-086-90	Sequence 90, Appl
21	68.6	13.7	290	10	US-09-815-242-4692	Sequence 4692, Ap
c 22	68.6	13.7	495	10	US-09-815-242-2687	Sequence 2687, Ap
c 23	68.6	13.7	495	10	US-09-815-242-2691	Sequence 2691, Ap
24	66.6	13.3	836	9	US-09-894-467-5	Sequence 5, Appli
25	66.4	13.3	76	10	US-09-974-300-4361	Sequence 4361, Ap
26	66.4	13.3	76	10	US-09-974-300-4403	Sequence 4403, Ap
27	66.4	13.3	76	10	US-09-974-300-4409	Sequence 4409, Ap
28	66.4	13.3	76	10	US-09-974-300-4418	Sequence 4418, Ap
29	66.4	13.3	76	10	US-09-974-300-8396	Sequence 8396, Ap
30	66.4	13.3	76	10	US-09-974-300-8438	Sequence 8438, Ap
31	66.4	13.3	76	10	US-09-974-300-8444	Sequence 8444, Ap
32	66.4	13.3	76	10	US-09-974-300-8453	Sequence 8453, Ap
c 33	66	13.2	9797	10	US-09-070-927A-550	Sequence 550, App
34	65.8	13.2	654	10	US-09-863-086-89	Sequence 89, Appl
35	65.6	13.1	246	10	US-09-863-086-95	Sequence 95, Appl
36	65.6	13.1	279	10	US-09-863-086-96	Sequence 96, Appl
37	65.2	13.1	2336	10	US-09-842-552-102	Sequence 102, App
38	64.4	12.9	74	10	US-09-974-300-4363	Sequence 4363, Ap
39	64.4	12.9	76	10	US-09-974-300-8398	Sequence 8398, Ap
c 40	63.6	12.7	1069	10	US-09-070-927A-869	Sequence 869, App
41	59.4	11.9	77	10	US-09-974-300-4362	Sequence 4362, Ap
42	59.4	11.9	77	10	US-09-974-300-4371	Sequence 4371, Ap
43	59.4	11.9	77	10	US-09-974-300-4377	Sequence 4377, Ap
44	59.4	11.9	77	10	US-09-974-300-4419	Sequence 4419, Ap
c 45	59.4	11.9	213	10	US-09-815-242-1374	Sequence 1374, Ap

ALIGNMENTS

RESULT 1  
US-09-790-988-1  
; Sequence 1, Application US/09790988  
; Patent No. US20020127687A1  
; GENERAL INFORMATION:  
; APPLICANT: SHIGENORU, SHUJI  
; APPLICANT: WATANABE, HIDEMI  
; APPLICANT: HATTORI, MASAHIRA  
; APPLICANT: SAKAKI, YOSHIYUKI  
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
; FILE REFERENCE: 081356/0159  
; CURRENT APPLICATION NUMBER: US/09/790, 988  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: JP2000-107160  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 640681  
; TYPE: DNA  
; ORGANISM: Buchnera sp.  
US-09-790-988-1

Query Match	19.8%	Score 98.8;	DB 10;	Length 640681;
Best Local Similarity	78.2%	Pred No. 5.6e-22;		
Matches 136;	Conservative 0;	Mismatches 27;	Indels 11;	Gaps 1;
QY 93	GGCTGTAGTCTCAGTTGGTTAGAGCGCACCCCTGTAGTAAGGGTTCAGGTCGCGAGTTCCAAAT 152			
Db 275641	GCCTTGTAGTCTCAGTTGGTTAGAGCGCACCCCTGTAGTAAGGGTTCAGGTCGCGAGTTCCAAAT 275700			
QY 153	CTGCCAGACCCACCAATTTGTCGGATGCGCAGTTCGAATGGGCGCATAGCTCAGCTGG 212			
Db 275701	CCACTCAGGCGTACCAAT-----AAAAAATCATCTGGGCTATAGCTCAGCTGG 275749			
QY 213	GAGAGCGCTGCTTTTCACGCGAGGAGTTCAGGATTCGATTCCTCTTGCCTCA 266			
Db 275750	GAGAGCGCTGCTTTTCACGCGAGGAGTTCAGGATTCGATTCCTCTTGCCTCA 275803			
RESULT 2				
US-09-863-086-87				

; Sequence 87, Application US/09863086  
; Patent No. US20020048762A1  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
; REGION BETWEEN THE 16S A  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/863,086  
; FILING DATE: 22-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/312,520  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/412,614  
; FILING DATE: 29-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.75USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/332-5300  
; TELEFAX: 612/332/9081  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 582 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: <Unknown>  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 87:  
US-09-863-086-87

Query Match 19.5%; Score 97.2; DB 10; Length 582;  
Best Local Similarity 75.8%; Pred. No. 3.6e-23;  
Matches 135; Conservative 0; Mismatches 38; Indels 5; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAAGGGTGAGGTGGCGGAGTTTCGAA 151  
|||||  
Db 98 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAAGGGTGAGGTGGCGGAGTTTCGAA 157  
|||||  
QY 152 TCTGCCAGACCCACCAAAATTTGCGGGATGCGGAGTGCATCAATGGGCCATAGCTCAGCTG 211  
|||||  
Db 158 TCAACCAAGACCCACCA-----GGTTCTTGAGAGGAAATGGGGGTGAGCTCAGCTG 212  
|||||  
QY 212 GGAGAGCGCTGCTTTGCACGAGGAGGTGAGGAGTTCGATCCTCTGCTCCACCA 269  
|||||  
Db 213 GGAGAGCGCTGCTTTGCACGAGGAGGTGATGTCGCGTTCGATCCCGTTCACCTCCACCA 270  
|||||

RESULT 3  
US-09-863-086-88  
; Sequence 88, Application US/09863086  
; Patent No. US20020048762A1  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi

; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
; REGION BETWEEN THE 16S A  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/863,086  
; FILING DATE: 22-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/312,520  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/412,614  
; FILING DATE: 29-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.75USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/332-5300  
; TELEFAX: 612/332/9081  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 590 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: <Unknown>  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 88:  
US-09-863-086-88

Query Match 19.5%; Score 97.2; DB 10; Length 590;  
Best Local Similarity 75.8%; Pred. No. 3.6e-23;  
Matches 135; Conservative 0; Mismatches 38; Indels 5; Gaps 1;  
QY 92 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAAGGGTGAGGTGGCGGAGTTTCGAA 151  
|||||  
Db 98 GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAAGGGTGAGGTGGCGGAGTTTCGAA 157  
|||||  
QY 152 TCTGCCAGACCCACCAAAATTTGCGGGATGCGGAGTGCATCAATGGGCCATAGCTCAGCTG 211  
|||||  
Db 158 TCAACCAAGACCCACCA-----GGTTCTTGAGAGGAAATGGGGGTGAGCTCAGCTG 212  
|||||  
QY 212 GGAGAGCGCTGCTTTGCACGAGGAGGTGAGGAGTTCGATCCTCTGCTCCACCA 269  
|||||  
Db 213 GGAGAGCGCTGCTTTGCACGAGGAGGTGATGTCGCGTTCGATCCCGTTCACCTCCACCA 270  
|||||

RESULT 4  
US-09-815-242-1358/c  
; Sequence 1358, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.



APPLICANT: Carr, Grant J.  
 APPLICANT: Yamamoto, Robert T.  
 APPLICANT: Xu, H. Howard  
 TITLE OF INVENTION: Identification of Essential Genes in  
 TITLE OF INVENTION: Prokaryotes  
 FILE REFERENCE: ELITRA.011A  
 CURRENT APPLICATION NUMBER: US/09/815,242  
 CURRENT FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 NUMBER OF SEQ ID NOS: 14110  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 1358  
 LENGTH: 243  
 TYPE: DNA  
 ORGANISM: Staphylococcus aureus  
 NAME/KEY: misc feature  
 LOCATION: (1)...(243)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-815-242-1358

Query Match 18.4%; Score 92; DB 10; Length 243;  
 Best Local Similarity 77.0%; Pred. No. 1.3e-21;  
 Matches 127; Conservative 0; Mismatches 31; Indels 7; Gaps 1;  
 QY 89 ATTGGGCTGTAGCTAGTGTGTTAGAGCGCACCCCTGATAAGGGTGTAGTGGCGAGTTC 148  
 Db 158 AATGGGCTATAGCTAGCTAGTGTGTTAGAGCGCACCCCTGATAAGGGTGTAGTGGTGC 99  
 QY 149 GAATCTGCCAGACCCACCAATTTGCGGATGCGCATGTCACAAATGGGCGCATAGCTCAG 208  
 Db 98 GAGTCNCCTTAGGCCACCATTT-----AATTTAATACCTATTGGGGGCTTAGCTCAG 46  
 QY 209 CTGGGAGAGCGCCTGCTTTGCACGCGAGGTCAGGAGTTCGATC 253  
 Db 45 CTGGGAGAGCGCCTGCTTTGCACGCGAGGTCAGGAGTTCGATC 1

RESULT 5  
 US-09-815-242-1377/c  
 Sequence 1377, Application US/09815242  
 Patent No. US20020061569A1  
 GENERAL INFORMATION:  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari L.  
 APPLICANT: Zyskind, Judith W.  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John D.  
 APPLICANT: Carr, Grant J.  
 APPLICANT: Yamamoto, Robert T.  
 APPLICANT: Xu, H. Howard  
 TITLE OF INVENTION: Identification of Essential Genes in  
 TITLE OF INVENTION: Prokaryotes  
 FILE REFERENCE: ELITRA.011A  
 CURRENT APPLICATION NUMBER: US/09/815,242  
 CURRENT FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/206,848  
 PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 NUMBER OF SEQ ID NOS: 14110  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 1377  
 LENGTH: 255  
 TYPE: DNA  
 ORGANISM: Staphylococcus aureus  
 US-09-815-242-1377

Query Match 18.3%; Score 91.4; DB 10; Length 255;  
 Best Local Similarity 77.0%; Pred. No. 2.1e-21;  
 Matches 127; Conservative 0; Mismatches 31; Indels 7; Gaps 1;  
 QY 89 ATTGGGCTGTAGCTAGTGTGTTAGAGCGCACCCCTGATAAGGGTGTAGTGGCGAGTTC 148  
 Db 158 AATGGGCTATAGCTAGCTAGTGTGTTAGAGCGCACCCCTGATAAGGGTGTAGTGGTGC 99  
 QY 149 GAATCTGCCAGACCCACCAATTTGCGGATGCGCATGTCACAAATGGGCGCATAGCTCAG 208  
 Db 98 GAGTCNCCTTAGGCCACCATTT-----AATTTAATACCTATTGGGGGCTTAGCTCAG 46  
 QY 209 CTGGGAGAGCGCCTGCTTTGCACGCGAGGTCAGGAGTTCGATC 253  
 Db 45 CTGGGAGAGCGCCTGCTTTGCACGCGAGGTCAGGAGTTCGATC 1

RESULT 6  
 US-09-815-242-1402/c  
 Sequence 1402, Application US/09815242  
 Patent No. US20020061569A1  
 GENERAL INFORMATION:  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari L.  
 APPLICANT: Zyskind, Judith W.  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John D.  
 APPLICANT: Carr, Grant J.  
 APPLICANT: Yamamoto, Robert T.  
 APPLICANT: Xu, H. Howard  
 TITLE OF INVENTION: Identification of Essential Genes in  
 TITLE OF INVENTION: Prokaryotes  
 FILE REFERENCE: ELITRA.011A  
 CURRENT APPLICATION NUMBER: US/09/815,242  
 CURRENT FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 NUMBER OF SEQ ID NOS: 14110  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 1402  
 LENGTH: 255  
 TYPE: DNA  
 ORGANISM: Staphylococcus aureus



; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1431  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1431

Query Match 18.3%; Score 91.4; DB 10; Length 255;  
Best Local Similarity 77.0%; Pred. No. 2.1e-21;  
Matches 127; Conservative 0; Mismatches 31; Indels 7; Gaps 1;  
QY 89 ATTGGGTCCTAGCTAGTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGGCAGTTC 148  
Db 158 AATGGGCTATAGCTAGCTAGCTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGGTGGTTC 99  
QY 149 GAATCTGCCAGACCCACCAATTTGTCGGGATGGCCAGTGTCAATATGGGGCCATAGCTCAG 208  
Db 98 GAGTCCACTTAGGCCACCACTT-----AATTTAATACCTATTTTGGGGCTTAGCTCAG 46  
QY 209 CTGGGAGAGCGCTGCTTTGCACGAGGTCAGGAGTTCGATC 253  
Db 45 CTGGGAGAGCGCTGCTTTGCACGAGGTCAGGAGTTCGATC 1

RESULT 10  
US-09-815-242-1454/c  
; Sequence 1454, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1454  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1454

Query Match 18.3%; Score 91.4; DB 10; Length 255;  
Best Local Similarity 77.0%; Pred. No. 2.1e-21;  
Matches 127; Conservative 0; Mismatches 31; Indels 7; Gaps 1;  
QY 89 ATTGGGTCCTAGCTAGTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGGCAGTTC 148  
Db 158 AATGGGCTATAGCTAGCTAGCTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGGTGGTTC 99  
QY 149 GAATCTGCCAGACCCACCAATTTGTCGGGATGGCCAGTGTCAATATGGGGCCATAGCTCAG 208  
Db 98 GAGTCCACTTAGGCCACCACTT-----AATTTAATACCTATTTTGGGGCTTAGCTCAG 46  
QY 209 CTGGGAGAGCGCTGCTTTGCACGAGGTCAGGAGTTCGATC 253  
Db 45 CTGGGAGAGCGCTGCTTTGCACGAGGTCAGGAGTTCGATC 1

RESULT 11  
US-09-815-242-1459/c  
; Sequence 1459, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1459  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1459

Query Match 18.3%; Score 91.4; DB 10; Length 255;  
Best Local Similarity 77.0%; Pred. No. 2.1e-21;  
Matches 127; Conservative 0; Mismatches 31; Indels 7; Gaps 1;  
QY 89 ATTGGGTCCTAGCTAGTGGTTAGAGCGCACCCCTGATAAGGTCAGGTCGGCAGTTC 148

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; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Holsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes

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/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14175
/ LENGTH: 255

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ORGANISM: Staphylococcus aureus  
US-09-815-242-1475

Query Match 18.3%; Score 91.4; DB 10; Length 255;  
Best Local Similarity 77.0%; Pred. NO. 2.1e-21;  
Matches 127; Conservative 0; Mismatches 31; Indels 7

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QY		
Db		
158	AATGGGCCCTATAGCTCAGCTGGTTAGACGCGCACCCCTGATAGCGTGAAGGTCGGTGGTTC	99
QY		
Db		
149	GAATCTGCCAGACACCACCAATTTTCGGGATGGCCAGTGTCAATGGGGCCATAGCTCAG	208
QY		
Db		
98	GAGTCACACTTAGGCCACCATT-----AATTTAATACCTATTTGGGGGCTTAGCTCAG	46
QY		
209	CTGGGAGAGCGCGCTGCTTTTCACGCGCAGGAGGTTCAGGATTCGATC	253
QY		
Db		
45	CTGGGAGAGCGCGCTGCTTTTCACGCGCAGGAGGTTCAGCGGTTTCGATC	1
Db		

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RESULT 14
US-09-815-242-1544/c
; Sequence 1544, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari L.
; APPLICANT: zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; PROKARYOTES
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21

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RESULT 15
US-09-815-242-1638/c
/ Sequence 1638, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ TITLE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1638
/ LENGTH: 255

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Query Match	18.3%;	Score 91.4;	DB 10;	Length 255;
Best Local Similarity	77.0%;	Prod. No. 2.1e-21;		
Matches 127;	Conservative 0;	Mismatches 31;	Indels 7	
89	ATTGGCTCTCTAGCTCAGTTGGTTAGAGCCACCCCTCATAAAGGTGAGGTGCGGCA			
158	AATGGGCGCTATAGCTCAGCTGGTTAGAGCGCACCCCTGATAAGCGTGAGGTCGGTGG			
149	GAATCTGCCGACACCCACCAATTTGTCGGGATGGCCAGTGTCAAATGGGGCCATAGCG			
98	GAGTCACCTAGGCCCCACCATT-----AATTTTAATACCTATTGTGGGGCGCTTAGCG			
209	CTGGGAGAGCGCCTGCTTTTCACGACGAGAGGTCAAGGAGTTCGATC			
45	CTGGGAGAGCGCCTGCTTTTCACGACGAGAGGTCAAGGAGTTCGATC			



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OM nucleic - nucleic search, using sw model

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Title: US-09-931-486-114

Perfect score: 499

Sequence: 1 ATCGAAGACTTCAGCTTCTT.....CAGATTGCTTGGGTATAT 499

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_esti.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	481.8	96.6	507	17	BH200120
C 2	480.2	96.2	629	17	BH201541
C 3	159	31.9	639	17	AQ509640
C 4	111.8	22.4	319	10	BE092111
C 5	86	17.2	754	17	BH405252
C 6	67.8	13.6	619	9	AA680996

C 7	67.4	13.5	593	17	BH400944
C 8	67.4	13.5	760	17	BH393190
C 9	65.6	13.1	6499	17	BH771024
C 10	65.4	13.1	712	17	BH397037
C 11	64.4	12.9	497	13	BI544108
C 12	64.4	12.9	548	13	BI544155
C 13	63.6	12.7	577	17	BH819575
C 14	62.8	12.6	539	13	BI544086
C 15	58.6	11.7	287	17	BH614410
C 16	58.4	11.7	191	17	AZ578476
C 17	54.2	10.9	617	9	AI526132
C 18	53.6	10.7	904	17	BH159957
C 19	53.2	10.7	2149	17	AQ012191
C 20	53	10.6	696	17	BH383241
C 21	52	10.4	216	17	BH169234
C 22	51.8	10.4	608	17	BH375641
C 23	51.6	10.3	579	17	BH375975
C 24	51.6	10.3	938	17	AZ683938
C 25	48.8	9.8	429	17	BH610380
C 26	48.6	9.7	197	17	BH855109
C 27	48.6	9.7	541	17	BH387664
C 28	47.8	9.6	429	17	BH789301
C 29	47.6	9.5	866	17	AZ542405
C 30	47.6	9.5	901	17	AZ531501
C 31	47.4	9.5	432	13	BI941477
C 32	47.2	9.5	704	17	BH427896
C 33	47.2	9.5	750	17	BH646171
C 34	47	9.4	612	17	AQ989869
C 35	47	9.4	963	17	AZ549906
C 36	46.4	9.3	895	17	BH131476
C 37	46	9.2	937	17	BH156063
C 38	45.8	9.2	984	17	BH680408
C 39	45.6	9.1	414	12	BF872471
C 40	45.6	9.1	702	17	BH586090
C 41	45.6	9.1	759	17	BH427885
C 42	45.6	9.1	969	17	BH147834
C 43	45.4	9.1	810	17	AZ679409
C 44	45.4	9.1	820	17	BH159532
C 45	45.4	9.1	822	17	AZ545581

## ALIGNMENTS

RESULT 1  
BH200120/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BH200120  
Sml-57J2.TF Sml Schistosoma mansoni genomic clone Sml-57J2, DNA  
sequence.  
BH200120  
BH200120.1 GI:16370164  
GSS.  
Schistosoma mansoni.  
Schistosoma mansoni  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.  
Shety,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed  
N.M.  
Use of end sequences from Schistosoma mansoni (Puerto Rico strain)  
Sml BAC library for gene discovery and map construction  
Unpublished (2001)  
Other\_GSSs: Sml-57J2.TF  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayedetigr.org  
lo.edu)  
Seq primer: M13 For  
Class: BAC ends.

BH400944 AG-ND-158  
BH393190 AG-ND-168  
BH771024 LIMGtag74  
BH397037 AG-ND-137  
BI544108 S071 Grac  
BI544155 S129 Grac  
BH819575 BACPP13-E  
BI544086 S042 Grac  
BH614410 1C22AG2 S  
AZ578476 23h03 Sho  
AI526132 pc3-2 Bll  
BH159957 ENT511TF  
AQ012191 430PIA043  
BH383241 AG-ND-137  
BH169234 SALK\_0008  
BH375641 AG-ND-133  
BH375975 AG-ND-133  
AZ683938 ENTJ28TR  
BH610380 SALK\_0088  
BH55109 SALK\_0866  
BH387664 AG-ND-157  
BH789301 SALK\_0017  
AZ542405 ENTER07TF  
AZ531501 ENTIC155TF  
BI941477 dg07g11.Y  
BH427896 BOHOK30TR  
BH646171 BOME267TF  
AQ989869 RfC00532  
AZ549906 ENTDN46TR  
BH131476 ENTNU96TF  
BH156063 ENTQT49TR  
BH680408 BOMKA39TF  
BF872471 IL3-ET011  
BH586090 BOHOC43TF  
BH427885 BOHOK30TF  
BH147834 ENTQM48TR  
AZ679409 ENTQO08TF  
BH159532 ENTXY12TR  
AZ545581 ENTGE06TR

FEATURES  
source Location/Qualifiers

1..507  
    /organism="Schistosoma mansoni"  
    /strain="Puerto Rico"  
    /db\_xref="taxon:6183"  
    /clone="Sml-57J2"  
    /clone\_lib="Sml"  
    /note=vector: pBelOAC11; Site 1: Hin dIII; Constructed in the laboratory of Dr. Denis Le Paslier at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBelOAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 x the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94."

BASE COUNT         136 a   129 c   117 g   125 t

ORIGIN

Query Match           96.6%; Score 481.8; DB 17; Length 507;  
Best Local Similarity 99.6%; Pred. No. 1.6e-141;  
Matches 483; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY       1   ATCGAAGACTTCAGCTTCTTTATAAGTCCACACGAATTCGTTGATTCACTTGCGAAAA 60  
        |||||  
DB       485 ATCAAAGACTCAGCTTCTTTATAAGTCCACACGAATTCGTTGATTCACTTGCGAAAA 426  
        |||||  
  
QY       61   GCgATTGGGTGAGACCCGAGAGTAGCATGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
        |||||  
DB       425 GCgATTGGGTGAGACCCGAGAGTAGCATGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 366  
        |||||  
  
QY       121 CCcCTGATAGGTTGAGGTGCGCAGTTCGAATTCGCCAGACCACCAATTCGCGGGATG 180  
        |||||  
DB       365 CCcCTGATAGGTTGAGGTGCGCAGTTCGAATTCGCCAGACCACCAATTCGCGGGATG 306  
        |||||  
  
QY       181 GCCAGTGTCAAATGGGGCCATAGCTCAGCTGGGAGAGCGCCTGTTGCACGACGAGGT 240  
        |||||  
DB       305 GCCAGTGTCAAATGGGGCCATAGCTCAGCTGGGAGAGCGCCTGTTGCACGACGAGGT 246  
        |||||  
  
QY       241 CAGGAGTTCGATCCTCTTGGCTCCACCATCACTCAGNCTCGCTGAAAGCTCAGAAAATG 300  
        |||||  
DB       245 CAGGAGTTCGATCCTCTTGGCTCCACCATCACTCAGNCTCGCTGAAAGCTCAGAAAATG 186  
        |||||  
  
QY       301 AACATTGGTAGTCCAATGTTGATTCTGTGGCTTTGGCCAGAGAAGTCTCTTTAAAAAATT 360  
        |||||  
DB       185 AACATTGGTAGTCCAATGTTGATTCTGTGGCTTTGGCCAGAGAAGTCTCTTTAAAAAATT 126  
        |||||  
  
QY       361 GGGTATGTGATAGAGTAGTAACAAGCGGTGTTTCACGTGACGTTGTTAATCAAGGCAAA 420  
        |||||  
DB       125 GGGTATGTGATAGAGTAGTAACAAGCGGTGTTTCACGTGACGTTGTTAATCAAGGCAAA 66  
        |||||  
  
QY       421 TTTGGGAGTTCAACGGCGAATTTTCGGGAATGTCGCTTTACGTTACGAATCTATAACC 480  
        |||||  
DB       65   TTTGGGAGTTCAACGGCGAATTTTCGGGAATGTCGCTTTACGTTACGAATCTATAACC 6  
        |||||  
  
QY       481 AGATT 485  
        |||||  
DB       5   AGATT 1

RESULT 2  
BH201541/c  
LOCUS BH201541  
DEFINITION Sml-57P13.TF Sml Schistosoma mansoni genomic clone Sml-57P13, DNA sequence.  
ACCESSION BH201541  
VERSION BH201541.1 GI:16373041  
KEYWORDS GSS.  
SOURCE Schistosoma mansoni.  
ORGANISM Schistosoma mansoni.  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;



Db 65 TTTCGAGTTCAAGCGGCAATTTTCGGCGAATGTCGTTCTACGTTACGAATCTATACC 6

QY 481 AGATT 485  
|||||

Db 5 AGATT 1

RESULT 3  
AQ509640/c  
LOCUS  
DEFINITION  
nbx0096P15f CUGI Rice BAC Library Oryza sativa genomic clone  
nbx0096P15f, DNA sequence.  
ACCESSION  
AQ509640  
VERSION  
AQ509640.1 GI:4733723  
KEYWORDS  
GSS.  
SOURCE  
Oryza sativa.  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE  
1. (bases 1 to 639)  
Wing,R.A. and Dean,R.A.  
A BAC End Sequencing Framework to Sequence the Rice Genome  
Unpublished (1998)  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Seq primer: TAATACGACTCCTATAGGG  
Class: BAC ends  
High quality sequence start: 86  
High quality sequence stop: 304.  
Location/Qualifiers  
1. .639  
/organism="Oryza sativa"  
/strain="Japonica"  
/cultivar="Nipponbare"  
/db\_xref="taxon:4530"  
/clone\_lib="CUGI Rice BAC Library"  
/tissue\_type="Leaf"  
/lab\_host="E. coli DH10B"  
/note="Vector: pBelobAC11; Site\_1: HindIII; Site\_2:  
HindIII; Rice is one of two most popular grains in the  
world. Half of the world population especially those  
inhabiting highly populated areas of the humid tropics  
and subtropics, rely on rice as their primary source of  
carbohydrate. Monocotyledonous rice is a diploid plant  
(2n=24) with a haploid genome equivalent of 431 Mbp  
(Arumuganathan and Earle, 1991). The relatively small  
genome of rice, three times larger than that of  
Arabidopsis, makes it suitable for genomic studies. In  
order to facilitate positional cloning, physical mapping  
and genome sequencing of rice, we have constructed a BAC  
library from Oryza sativa, Nipponbare variety. The  
library contains 36,864 clones with an average insert size  
of 128.5 kb providing 10.9 haploid genome equivalents. The  
deep coverage allows the isolation a particular sequence  
with a probability of 99.9 %. Two high density filters,  
each containing 18,432 clones (doubly spotted), represent  
the whole library for colony screening."  
BASE COUNT 158 a 175 c 148 g 156 t 2 others  
ORIGIN

Query Match 31.9%; Score 159; DB 17; Length 639;  
Best Local Similarity 71.2%; Pred. No. 3.7e-39;  
Matches 327; Conservative 0; Mismatches 85; Indels 47; Gaps 7;

QY 33 CACGAATTGCTGATTCACTTGCAGAAAGCGATTGGTTGAGA-----CCCGAGAGTGAC 87  
|||||

Db 639 CACGAATTGCTTTATTTCACGTATAGAAGAGCAATTGAGTTAGATAGACTCAAGGTAAGAC 580

QY 88 GATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGTGAGTGGCGAGTT 147  
|||||

Db 579 GATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGGGTGAGTGGCGAGTT 520  
|||||

QY 148 CGAATCTGCCAGACCCACCAATTTGTCGGGATGCCAGTGTCAAAATGGGCGCATAGCTCA 207  
|||||

Db 519 CGAATCTGCCAGACCCACCA-----TCGATGGGGCCCATAGCTCA 478  
|||||

QY 208 GCTGGGAGAGCGCTGTTGTCAGCGAGGAGTTCAGAGTTCGATCTCTCTGGCTCCAC 267  
|||||

Db 477 GCTGGGAGAGCGCTGCTTGCACGAGGAGTTCAGAGTTCGATCTCTCTGGCTCCAC 418  
|||||

QY 268 CATC-----AACTCAGCATCGCTGAAAGCTCAGAAATGAACATT-GGTA 310  
|||||

Db 417 CATCTCCACCCTGTGCGATAACACGATTGTTGAAAGCTCAGAAATGAGTGTCCCTT 358  
|||||

QY 311 GTTCAATGTTGATTCTGGTCTTTGCGCCAGAACTGTTCTTTAAAAATTTGGGTATGTA 370  
|||||

Db 357 GCGGAATCTGACITCTGGTCTTTG-ATCAGAACTGTTCTTTAAAAAATTTGGGAAAGTGA 299  
|||||

QY 371 TAGAAGT-----GACTAACAGCGTGTTCACCTGACAGTGTTAATCAAGGCAAAATTTGC 425  
|||||

Db 298 TAGAAGTAGACACATTTGACTGTTTTCACCTGGCAGTGCATGTCGTCAGAGTAAATCTTGC 239  
|||||

QY 426 GAGTTCAAGCGCAATTTTCGGCG-AAATGTCGTTCTTTCAC 463  
|||||

Db 238 GAATCAAGCGCAAGTTTTCGGCGAATGTCGTTCTTTCAC 200  
|||||

RESULT 4  
BE092111 319 bp mRNA linear EST 12-JUN-2000  
LOCUS  
DEFINITION  
IL2-BT0733-240400-073-G03 BT0733 Homo sapiens cDNA, mRNA sequence.  
ACCESSION  
BE092111  
VERSION  
BE092111.1 GI:8482563  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
1 (bases 1 to 319)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
,M.J., Soares,F., Brentani,L.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
JOURNAL  
20202663  
MEDLINE  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=IL2-BT0733-240  
400-073-G03&t3=2000-04-24&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 298.  
Location/Qualifiers  
1. .319  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="BT0733"  
/dev\_stage="Adult"

FEATURES  
source

/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 73 a 62 c 91 g 93 t

ORIGIN

Query Match 22.4%; Score 111.8; DB 10; Length 319;  
Best Local Similarity 81.7%; Pred. NO. 2.3e-24;  
Matches 143; Conservative 0; Mismatches 27; Indels 5; Gaps 1;

QY 105 AGTTGGTTAGAGCGCCCTGATAGGGTGGAGTGGCGAGTTCGAATCTGCCAGACCC 164

Db 1 AGTTGGTTAGAGCGCCCTGATAGGGTGGAGTGGCGAGTTCGAATCTGCCAGACCC 60

QY 165 ACCAATGT-----CGGGATGGCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCG 219

Db 61 ACCAATCTTGTGGCGGAAAGCGCTAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCG 120

QY 220 CTTGCTTTGCACGAGAGTTCAGGAGTTCGATCCTCTGGCTCCACCATCAAC 274

Db 121 CTTGCTTTGCACGAGAGTTCAGGAGTTCGATCCTCTGGCTCCACCATTTAC 175

RESULT 5

BH405252/c

LOCUS

DEFINITION AG-ND-127K13.TR ND-TAM Anopheles gambiae genomic clone AG-ND-127K13 , DNA sequence.

ACCESSION

VERSION BH405252

KEYWORDS

SOURCE BH405252.1 GI:17351468

ORGANISM

African malaria mosquito.

REFERENCE

AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.

TITLE Direct Submission of BAC-end sequences from Anopheles gambiae

JOURNAL Unpublished (2001)

COMMENT

Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543  
Email: b.loftus@tigr.org  
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.  
Seq primer: M13 Rev  
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..754

/organism="Anopheles gambiae"

/strain="PEST"

/db\_xref="taxon:7165"

/clone="AG-ND-127K13"

/clone\_lib="ND-TAM"

/note="Vector: pECBAC1; Site\_1: HindIII"

180 a 199 c 167 g 208 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 156; Conservative

0; Mismatches 70; Indels 8; Gaps 2;

QY 66 TGGGTTGAGACCGGAGAGTGAACGATTGGGTCTGTAGCTCAGTTGGTTAGACGCGACCCCT 125

Db 663 TGGCCTGGGTGCAGGGTGGCTGGGACTGGTCTGTAGCTCAGCTGGTTAGACGCGCTCTT 604

QY 126 GATAAGGGTGAAGTCCGCGAGTTCGAATCTGCCAGACCCACCA-----ATTGTCGGGA 178

Db 603 GATAAGCGGGGGTGGTTCGAGCCCACTAGACCCACCAAGATTCCCAATGCTGGT 544

QY 179 TGGCCAGTGTCAAAATGGGGCCATAGCTCAGC-TGGGAGAGCGCTGCTTTGCACGCGAGGA 237

Db 543 TGTCTGAGGATCCCGCGGGGATAGCTCAGCTTGGGAGAGCAGCTGCTTTGCAAGCAGGG 484

QY 238 GGTCTGAGGATTCGATCCTCTTGGCTCCACCATCACTCAGTCGTCGTAAGC 291

Db 483 GGTCTGCGTTCGATCCCTCATCTCCACCAAGATCGCTGGTGGCAACAAGC 430

RESULT 6

AA680996/c

LOCUS

DEFINITION SW3D9CA514SK Brugia malayi L3 molting-day 9 larva CDNA (SAW97MLW-BmL3d9) Brugia malayi CDNA clone SW3D9CA514 5', mRNA sequence.

ACCESSION

VERSION AA680996

KEYWORDS

SOURCE AA680996.1 GI:2663001

ORGANISM

Brugia malayi.

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Steven A. Williams

Molecular Parasitology

Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA

Tel: 4135853826

Fax: 4135853786

Email: genomesmith.edu

Seq primer: pbuescript SK.

Location/Qualifiers

1..619

/organism="Brugia malayi"

/db\_xref="taxon:6279"

/clone="SW3D9CA514"

/clone\_lib="Brugia malayi L3 molting-day 9 larva CDNA (SAW97MLW-BmL3d9)"

/dev\_stage="third stage larvae, nine days after infection"

/lab\_host="E. coli XL1-Blue MRF"

/note="Vector: LambdaZap II (Unizap XR); Site\_1: Eco RI (5' end); Site\_2: Xho I (3' end); Brugia malayi is a lymphatic filarial nematode parasite of humans. mRNA was prepared from third stage larvae of Brugia malayi isolated from the peritoneal cavity of jirds nine days after infection. The mRNA was converted to double stranded cDNA using reverse transcriptase and oligo (dT) followed by Ruase H and DNAPol I. The library was constructed by Michelle Lizotte-Waniewski. The library is available from the Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, MA 01063 USA phone +1 413 585-3826 fax +1 413 585-3786 email genomesmith.edu"

148 a 148 c 121 g 168 t

BASE COUNT

ORIGIN

```

Query Match      13.6%; Score 67.8; DB 9; Length 619;
Best Local Similarity 68.6%; Pred. No. 2.9e-10;
Matches 129; Conservative 0; Mismatches 40; Indels 19; Gaps 2;

QY 103 TCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGTTCGCGCATCTGGAATCTGCCAGAC 162
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 518 TCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGTTCGCGCATCTGGAATCTGCCAGAC 459
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 163 CCACCAATTGTC-----GGGATGCCAGTCTCAATGGGCGCCATAGCT 205
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 458 CTACCAAAATTCACGGCAAAATTTGAAGAGGTTTAACTACATGCTATGGGTTATAGCT 399
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 206 CAGCTGGGAGAGCGCTGTTTGA--CGCAGGAGTTCAGGATTCGATCCTCTGGCT 263
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 398 CAGCTGGGAGAGCGCTGTTTGCATCGCAGGAGTNCNCGTTGATCCCGCWTNGCT 339
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 264 CCACCATC 271
      ||||| |||||
Db 338 CCACCATC 331
      ||||| |||||

RESULT 7
BH400944/c
LOCUS BH400944
DEFINITION AG-ND-158022.TF ND-TAM Anopheles gambiae genomic clone AG-ND-158022
, DNA sequence.
ACCESSION BH400944
VERSION BH400944.1 GI:17347147
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 593)
AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other GSSs: AG-ND-158022.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.

FEATURES
source
1..593
Location/Qualifiers
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-158022"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"

BASE COUNT 119 a 157 c 118 g 199 t
ORIGIN

Query Match      13.5%; Score 67.4; DB 17; Length 593;
Best Local Similarity 71.9%; Pred. No. 3.8e-10;
Matches 123; Conservative 0; Mismatches 31; Indels 17; Gaps 2;

QY 98 GTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGTTCGCGCATCTGCC 157
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 569 GTAGCTCAGTTGGTTAGAGCGCTACACTGATATGTAGAGTTCGCGCATCTGCC 510
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 158 CAGACCCCAATTTGCGGGATGGCCAGTGTCAATGGGCGCCATAGCTCAGCTGGG-AGA 216
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 509 CGAGACTACTAATTGA-----AAAAGGGGAATTAGCTCAGCTGGCTAGA 466
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 217 GGCCTGCTTTTCACGACGAGGTTCAGAGTTCGATCCTCTCTGGCTCCAC 267
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 574 GTAGCTCAGCTGGTTAGAGCGCTACACTGATATGTAGAGTTCGCGCATCTGCC 515
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QY 158 CAGACCCCAATTTGTCGGGATGGCCAGTGTCAAAATGGGCGCCATAGCTCAGCTGGG-AGA 216
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 514 CGAGACTACTAATTGA-----AAAAGGGGAATTAGCTCAGCTGGCTAGA 471
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 217 GGCCTGCTTTTCACGACGAGGTTCAGAGTTCGATCCTCTCTGGCTCCAC 267
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 GGCCTGCTTTTCACGACGAGGTTCAGAGTTCGACTCCCTTATTCTCCAC 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
BH393190/c
LOCUS BH393190
DEFINITION AG-ND-168H12.TR ND-TAM Anopheles gambiae genomic clone AG-ND-168H12
, DNA sequence.
ACCESSION BH393190
VERSION BH393190.1 GI:17339331
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 760)
AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other GSSs: AG-ND-168H12.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 Rev
Class: BAC ends.

FEATURES
source
1..760
Location/Qualifiers
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-168H12"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"

BASE COUNT 171 a 187 c 139 g 263 t
ORIGIN

Query Match      13.5%; Score 67.4; DB 17; Length 760;
Best Local Similarity 71.9%; Pred. No. 4.4e-10;
Matches 123; Conservative 0; Mismatches 31; Indels 17; Gaps 2;

QY 98 GTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGTTCGCGCATCTGCC 157
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 569 GTAGCTCAGTTGGTTAGAGCGCTACACTGATATGTAGAGTTCGCGCATCTGCC 510
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 158 CAGACCCCAATTTGCGGGATGGCCAGTGTCAATGGGCGCCATAGCTCAGCTGGG-AGA 216
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 509 CGAGACTACTAATTGA-----AAAAGGGGAATTAGCTCAGCTGGCTAGA 466
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QY 217 GGCCTGCTTTTCACGACGAGGTTCAGAGTTCGATCCTCTCTGGCTCCAC 267
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



RESULT	13
LOCUS	BH819575
DEFINITION	BACPP13-E14.y Pristionchus pacificus BAC ends Pristionchus pacificus genomic, DNA sequence.
ACCESSION	BH819575
VERSION	BH819575.1 GI:20993843
KEYWORDS	GSS.
SOURCE	Pristionchus pacificus.
ORGANISM	Pristionchus pacificus. Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE	1 (bases 1 to 577)
AUTHORS	Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R., Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A., Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
TITLE	A BAC-based genetic linkage map of the nematode Pristionchus pacificus
JOURNAL	Unpublished (2002)
COMMENT	Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

Class: BAC ends.

#### FEATURES

Source

Location/Qualifiers

1..577

/organism="Pristionchus pacificus"

/strain="var. California"

/db\_xref="taxon:54126"

/clone\_lib="Pristionchus pacificus BAC ends"

129 a 142 c 139 g 167 t

#### BASE COUNT

ORIGIN

Query Match 12.7%; Score 63.6; DB 17; Length 577;

Best Local Similarity 66.7%; Pred. No. 6e-09;

Matches 128; Conservative 0; Mismatches 49; Indels 15; Gaps 2;

QY 92 GGCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGAGGTGAGGTGCGGAGTTCGAA 151

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Db 4 GGGCTATAGCTCAGCTGAG-GAGAGCGCTTGATGGCATGCAAGAGGTGAGCGGTTTCGAT 62

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QY 152 TCTGCCAGACCCACCAATTGTCTG-----GGATGGCCAGTGTCAAAATGGGG 197

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Db 63 CCGCTTAGCTCCACCAATTTTGACCCAGCAAACTTGGTACGTAAACGCATCGTGGG 122

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QY 198 CCATAGCTCAGCTGGAGAGCGCTCTTTGACGAGGAGGTGAGGATTCGATCTCC 257

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Db 123 CTATAGCTCAGCTGGAGAGCGCTTGATGGCATGCAAGAGGTGAGCGGTTTCGATCCGC 182

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QY 258 TTGGCTCCACCA 269

||||| |||||||

Db 183 TTAGCTCCACCA 194

#### RESULT 14

BI544086

LOCUS

DEFINITION S042 Gracillaria lemaneiformis gametophyte cdna library Gracillaria

lemaneiformis cdna 5', mRNA sequence.

ACCESSION BI544086

VERSION BI544086.1 GI:19033768

KEYWORDS EST.

SOURCE Gracillaria lemaneiformis.

ORGANISM Gracillaria lemaneiformis

Eukaryota; Rhodophyta; Florideophyceae; Gracillariales;

Gracillariaceae; Gracillaria.

REFERENCE 1 (bases 1 to 539)

AUTHORS Sun,X., Yang,G.P., Mao,Y.X. and Zhang,X.C.

TITLE Analysis of expressed sequence tags of a marine red alga,

Gracillaria lemaneiformis

Unpublished (2001)

JOURNAL Contact: Sun, X.; Zhang, X. C.

COMMENT College of Marine Life Sciences

Ocean University of Qingdao

Yushan Road 5, Qingdao, 266003, Shandong, China

Tel: +86-0532-2032789

Fax: +86-0532-2032276

Email: xc.zhang@ouqd.edu.cn

PCR Primers

FORWARD: 5' -CGTGATACCTGCTAGAGT-3'

BACKWARD: 5' -CTGATCTAGACCTGCGGCTC-3'

Seq primer: 5' -CGTGATACCTGCTAGAGT-3'

POLYA=Yes.

Location/Qualifiers

1..539

/organism="Gracillaria lemaneiformis"

/db\_xref="taxon:2778"

/clone\_lib="Gracillaria lemaneiformis gametophyte cdna

library"

/tissue\_type="gametophyte thalli"

/note="Vector: pMD 18-T; Site 1: EcoR V with a T hang;

Wild type Gracillaria lemaneiformis were harvested from

Zhanshan Bay, Qingdao (China). After rinsed with boiled

seawater, younger thalli was cut and washed every 3-4

days until 1 month. Then thalli was cultivated in

Provasoli medium. Total RNA was isolated from thalli of gametophyte algae, using UNIQ-10 Trizol Total RNA Preparation Kit(Sangon Inc., Shanghai, China). The cDNA was synthesized, amplified and cloned using cDNA Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector (Takara Biotechnology Co., Ltd., Dalian, China), respectively."

BASE COUNT 179 a 89 c 109 g 162 t

#### ORIGIN

Query Match

Best Local Similarity

Matches 118; Conservative

0; Mismatches 47; Indels 17; Gaps 1;

QY 92 GGCTCTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGAGGTGAGGTGCGGAGTTCGAA 151

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 66 GGCTTATTAGCTCAGTTGGTTAGAGCGCACCCCTGTATAGAGGTGAGGTGCGGAGTTCGAA 125

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 152 TCTGCCAGACCCACCAATTGTCTGCGGATGCGCATGTCAAATGGGCGCATAGCTCAGCTG 211

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 126 TCCAGGATAGCCACCA-----TGAATAAGGGGGGTATAGCTCAGCTG 168

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 212 GGAGAGCGCTCTGTTGACGACGAGGTCAGGAGTTCGATCCTCTGGCTCCACCATC 271

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 169 GTAGAGTGTCTGCTTTTGCAAGGCGATGTGAGCGGTTCAATCCGCTTATCTCCAAGTTT 228

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 272 AA 273

|||||

Db 229 AA 230

|||||

#### RESULT 15

BI614410

LOCUS

DEFINITION

1C22AG2 Subclones from overlapping BAC clones spanning the hrp

cluster of Erwinia carotovora subsp. atroseptica Pectobacterium

carotovorum subsp. atrosepticum genomic, DNA sequence.

ACCESSION BI614410

VERSION BI614410.1 GI:18078210

KEYWORDS GSS.

SOURCE Pectobacterium carotovorum subsp. atrosepticum.

ORGANISM Pectobacterium carotovorum subsp. atrosepticum

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

Pectobacterium.

REFERENCE 1 (bases 1 to 287)

AUTHORS Bell,K.S., Avrova,A.O., Holeva,M.C., Cardie,L., Morris,W., De Jong

W., Toth,I.K., Waugh,R., Bryan,G.J. and Birch,P.R.J.

TITLE Sample sequencing of a selected region of the genome of Erwinia

carotovora subsp. atroseptica reveal candidate phytopathogenicity

genes and allows comparison with Escherichia coli

Unpublished (2002)

JOURNAL Contact: Bell KS

COMMENT Scottish Crop Research Institute

Invergowrie, Dundee, United Kingdom, DD2 5DA

Email: khell@scri.sari.ac.uk

Class: BAC subclone.

Location/Qualifiers

1..287

/organism="Pectobacterium carotovorum subsp. atrosepticum"

/strain="SCR1039"

/db\_xref="taxon:29471"

/clone\_lib="Subclones from overlapping BAC clones spanning

the hrp cluster of Erwinia carotovora subsp. atroseptica"

/note="vector: pGEM 3zf; DNA from BAC clones Eca2B8 and

Eca1C22 was nebulised and cloned into pGEM 3zf and

sequenced with SP6 or T7 primers"

BASE COUNT 74 a 62 c 78 g 73 t

#### ORIGIN

Query Match

Best Local Similarity

Matches 67; Conservative

0; Mismatches 14; Indels 0; Gaps 0;

us-09-931-486-114.rst

Qy	93	GGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAGTCCGCGAGTTCGAAT	152
Db	174	GGCTGTGTAGCTCAGTGGTTAGAGCGCACCCCTGATAAGGGTGAGTTCGTTCAAGT	233
Qy	153	CTGCCACAGACCCACCAATTGT	173
Db	234	CCACTCAGGCCTACCAAAATTT	254

Search completed: February 1, 2003, 04:22:05  
Job time : 936.115 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:06:21 ; Search time 963.563 Seconds  
(without alignments)  
14135.156 Million cell updates/sec

Title: US-09-931-486-115

Perfect score: 468

Sequence: 1 ATCGACGACATCAGCTGTCT.....CAGATTGCTGGGTTATAT 468

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*\*

1: gb\_ba:\*\*

2: gb\_hgt:\*\*

3: gb\_in:\*\*

4: gb\_om:\*\*

5: gb\_ov:\*\*

6: gb\_pat:\*\*

7: gb\_ph:\*\*

8: gb\_pl:\*\*

9: gb\_pr:\*\*

10: gb\_ro:\*\*

11: gb\_sts:\*\*

12: gb\_sy:\*\*

13: gb\_un:\*\*

14: gb\_vi:\*\*

15: em\_ba:\*\*

16: em\_fun:\*\*

17: em\_hum:\*\*

18: em\_in:\*\*

19: em\_mu:\*\*

20: em\_om:\*\*

21: em\_or:\*\*

22: em\_ov:\*\*

23: em\_pat:\*\*

24: em\_ph:\*\*

25: em\_pl:\*\*

26: em\_ro:\*\*

27: em\_sts:\*\*

28: em\_un:\*\*

29: em\_vi:\*\*

30: em\_htg\_hum:\*\*

31: em\_htg\_inv:\*\*

32: em\_htg\_other:\*\*

33: em\_htg\_mus:\*\*

34: em\_htg\_pln:\*\*

35: em\_htg\_rod:\*\*

36: em\_htg\_mam:\*\*

37: em\_htg\_vrt:\*\*

38: em\_sy:\*\*

39: em\_htgo\_hum:\*\*

40: em\_htgo\_mus:\*\*

41: em\_htgo\_other:\*\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	468	100.0	468	6	A48048	A48048 Sequence 11
2	468	100.0	468	6	ARI77093	ARI77093 Sequence
3	468	100.0	468	6	AX191056	AX191056 Sequence
4	297.8	63.6	527	1	AF127584	AF127584 Pseudomon
5	296	63.2	527	1	AF127586	AF127586 Pseudomon
6	290.8	62.1	526	1	AF127583	AF127583 Pseudomon
7	288.4	61.6	521	1	AF364305	AF364305 Pseudomon
8	288.4	61.6	521	1	AF364307	AF364307 Pseudomon
9	286.4	61.2	523	1	AF364308	AF364308 Pseudomon
10	285.2	60.9	541	1	AF127582	AF127582 Pseudomon
11	283.6	60.6	541	1	AF127580	AF127580 Pseudomon
12	278.4	59.5	543	1	AF127590	AF127590 Pseudomon
13	277.6	59.3	526	1	AF127585	AF127585 Pseudomon
14	276.4	59.1	540	1	AF127581	AF127581 Pseudomon
15	275.8	58.9	584	1	AF127570	AF127570 Alcanivor
16	275.8	58.9	584	1	AF127571	AF127571 Alcanivor
17	274.4	58.6	539	1	AF127578	AF127578 Pseudomon
18	274.4	58.6	539	1	AF127579	AF127579 Pseudomon
19	273.8	58.5	5679	1	AF134704	AF134704 Pseudomon
20	273.6	58.5	525	1	AF127591	AF127591 Pseudomon
21	273.6	58.5	567	1	PSERGDNNA	L06304 Pseudomonas
22	273.6	58.5	567	1	PSERGDNNA	L06306 Pseudomonas
23	272.2	58.2	488	1	PCI279242	AJ279242 Pseudomon
24	267.8	57.2	588	6	BD011675	BD011675 Method fo
25	267.8	57.2	588	23	E49505	E49505 Method for
26	265.4	56.7	555	1	AF148208	AF148208 Pseudomon
27	262.4	56.1	462	1	PAG279243	AJ279243 Pseudomon
28	262	56.0	543	1	AF127588	AF127588 Pseudomon
29	261.2	55.8	562	1	PSERGDNAB	L06307 Pseudomonas
30	259.6	55.5	562	1	PSERGDNAB	L06305 Pseudomonas
31	258.4	55.2	522	1	AF127587	AF127587 Pseudomon
32	257.4	55.0	631	1	AF422499	AF422499 Unculture
33	257.4	55.0	631	1	AF422501	AF422501 Unculture
34	242.2	51.8	4958	1	AF134705	AF134705 Pseudomon
35	239.8	51.2	553	1	D87087	D87087 Pseudomonas
36	231	49.4	667	1	AY119683	AY119683 Pseudomon
37	226.8	48.5	564	1	D86357	D86357 Pseudomonas
38	225.8	48.2	557	1	AF127589	AF127589 Pseudomon
39	221.6	47.4	529	1	PST251904	AJ251904 Pseudomon
40	221.6	47.4	529	1	PST390587	AJ390587 Pseudomon
41	220.4	47.1	521	1	PAB439389	AJ439389 Pseudomon
42	219.6	46.9	578	1	D86378	D86378 Pseudomonas
43	219.2	46.8	528	1	PAB439391	AJ439391 Pseudomon
C 44	219.2	46.8	1176	1	AE004949	AE004949 Pseudomon
C 45	219.2	46.8	12065	1	AE004883	AE004883 Pseudomon

## ALIGNMENTS

RESULT 1  
A48048  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

A48048  
Sequence 115 from Patent WO9600298.  
A48048  
A48048.1 GI:2301910  
unidentified.  
unidentified.  
unclassified.  
1 (bases 1 to 468)  
James G., Rossal, R. and van, H.H.  
SIMULTANEOUS DETECTION, IDENTIFICATION AND DIFFERENTIATION OF  
EUBACTERIAL TAXA USING A HYBRIDIZATION ASSAY  
Patent: WO 9600298-A 115 04-JAN-1996;

468 bp  
DNA  
linear  
PAT 07-MAR-1997

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INNOGENETICS NV (BE)
Other publication AU 2924695 960119.
Location/Qualifiers
1. 468
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 117 a 101 c 117 g 133 t
ORIGIN
Query Match 100.0%; Score 468; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.5e-122;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGAGCATCAGCTGTCTCATAAGCTCCACACGAAATTCGTTGATTTCATTGAAGAAGA 60
CGATTAGGTTAGCAACCTTCGATTGGTCTGTAGCTCAGTTCAGTTGGTTAGAGCGCACCCCTGA 120
DB 61 CGATTAGGTTAGCAACCTTCGATTGGTCTGTAGCTCAGTTCAGTTGGTTAGAGCGCACCCCTGA 120
CGATTAGGTTAGCAACCTTCGATTGGTCTGTAGCTCAGTTCAGTTGGTTAGAGCGCACCCCTGA 120
QY 121 TAAGGTGAGGTGGCGAGTTCGAATTCGCCACAGACCCACCAATTCGTTGGGCGCATAGCT 180
TAAGGTGAGGTGGCGAGTTCGAATTCGCCACAGACCCACCAATTCGTTGGGCGCATAGCT 180
DB 121 TAAGGTGAGGTGGCGAGTTCGAATTCGCCACAGACCCACCAATTCGTTGGGCGCATAGCT 180
TAAGGTGAGGTGGCGAGTTCGAATTCGCCACAGACCCACCAATTCGTTGGGCGCATAGCT 180
QY 181 CAGCTGGGAGAGCGCTGCTTCACAGCAGGAGGTTCAGCGGTTCCGATCCCGCTTGGCTCC 240
CAGCTGGGAGAGCGCTGCTTCACAGCAGGAGGTTCAGCGGTTCCGATCCCGCTTGGCTCC 240
DB 181 CAGCTGGGAGAGCGCTGCTTCACAGCAGGAGGTTCAGCGGTTCCGATCCCGCTTGGCTCC 240
CAGCTGGGAGAGCGCTGCTTCACAGCAGGAGGTTCAGCGGTTCCGATCCCGCTTGGCTCC 240
QY 241 ACCACCCCGCTTCCAGAGTTTGTCAAAAGCTTAGAAATGAATATTCGCGTCGAATATTGATT 300
ACCACCCCGCTTCCAGAGTTTGTCAAAAGCTTAGAAATGAATATTCGCGTCGAATATTGATT 300
DB 241 ACCACCCCGCTTCCAGAGTTTGTCAAAAGCTTAGAAATGAATATTCGCGTCGAATATTGATT 300
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TCTGAACCTTATCAGAAATCGTCTTTAAAAATTTGGGTATGTGATAGAAAGATAGACTGG 360
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ACAGCACTTTCAGTGTGTGTTCAGGCTTAAGTAAAAATTTCTGAGTAATTAACAAGTTT 420
DB 361 ACAGCACTTTCAGTGTGTGTTCAGGCTTAAGTAAAAATTTCTGAGTAATTAACAAGTTT 420
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TGGCGAAATGTGTCTTCACAGTATACCAAGATTGCTTGGGGTTATAT 468
DB 421 TGGCGAAATGTGTCTTCACAGTATACCAAGATTGCTTGGGGTTATAT 468
TGGCGAAATGTGTCTTCACAGTATACCAAGATTGCTTGGGGTTATAT 468

RESULT 3
AX191056
LOCUS
DEFINITION Sequence 115 from Patent EP1091004.
ACCESSION AX191056
VERSION AX191056.1 GI:15149701
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 468)
AUTHORS James G., Rossau, R. and Van Heuverswyn, H.
TITLE Simultaneous detection, identification and differentiation of
eubacterial taxa using a hybridization assay
JOURNAL Patent: EP 1091004-A 115 11-APR-2001;
INNOGENETICS N.V. (BE)
FEATURES
source Location/Qualifiers
BASE COUNT 117 a 101 c 117 g 133 t
ORIGIN
Query Match 100.0%; Score 468; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.5e-122;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DEFINITION Sequence 115 from patent US 6312903.
ACCESSION ARI77093
VERSION ARI77093.1 GI:17919448
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 468)
AUTHORS James G., Rossau, R. and Van Heuverswyn, H.
TITLE Simultaneous detection, identification and differentiation of
eubacterial taxa using a hybridization assay
JOURNAL Patent: US 6312903-A 115 06-NOV-2001;
INNOGENETICS N.V. (BE)
FEATURES
source Location/Qualifiers
BASE COUNT 117 a 101 c 117 g 133 t
ORIGIN
Query Match 100.0%; Score 468; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.5e-122;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	169	-----GGGGCCATAGCTCAGCTGGGAGAGCGGCTGCCCTGCACGAGGAGTTCAG	218
Db	191	GTAGCAATACGGGCCATAGCTCAGCTGGGAGAGCGGCTGCCCTGCACGAGGAGTTCAG	250
QY	219	CGTTTCGATCCCGTGGCTCCACCGCCGCTTGCAGTTTGCACAGCTTAGAATGA	278
Db	251	CGTTTCGATCCCGTGGCTCCACCGCCGCTTGCAGTTTGCACAGCTTAGAATGA	310
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QY	329	AAATTTGGGTATGTAGTAAAGATAGACTGGACAGCACTTCACTGGTGTGTTTCAGG	388
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QY	389	CTAAGTAAATTTGTGAG--TAATTACAAAGTTTTCGGCGAATGTTGCTTTCACAGTATA	446
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QY	447	ACCAGATTGCTGGGGTTATAT 468	
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RESULT 6			
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LOCUS	AF127583	526 bp DNA linear BCT 10-MAR-2001	
DEFINITION	Pseudomonas gingeri strain pf2 16S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; trna-ile and trna-ala genes, complete sequence; and 23S ribosomal RNA gene, partial sequence.		
ACCESSION	AF127583.1	GI:13270381	
VERSION			
KEYWORDS			
SOURCE	Pseudomonas gingeri.		
ORGANISM	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.		
REFERENCE	1 (bases 1 to 526)		
AUTHORS	Kwon, S.W. and Cheon, M.S.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-FEB-1999) Division of Molecular Genetics, National Institute of Agricultural Science and Technology, Seodun-dong 249, Suwon, Kyunggi-do 441-707, Republic of Korea		
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	Matches 403; Conservative 0; Mismatches 62; Indels 35; Gaps 4;		
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Db	372	AAATTTGGGTATGTAGTAAAGATAGACTGAACTGCTTCACTGTTCAACGGATCAGG	431
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DEFINITION	Pseudomonas tolaasii LMG 6641 internal transcribed spacer 1, complete sequence.		
ACCESSION	AF364306		
VERSION	AF364306.1	GI:13926167	
KEYWORDS			
SOURCE	Pseudomonas tolaasii.		
ORGANISM	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.		
REFERENCE	1 (bases 1 to 521)		
AUTHORS	Munsch, P. and Alatosava, T.		
TITLE	ITS 1 internal transcribed spacer		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 521)		
AUTHORS	Munsch, P. and Alatosava, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-MAR-2001) REDEC of Kajaani, Biotechnology Laboratory, University of Oulu, Salmelantie 43, Sotkamo 88600, Finland		
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Query Match 61.6%; Score 288.4; DB 1; Length 521;  
 Best Local Similarity 79.8%; Pred. No. 5.9e-71;  
 Matches 410; Conservative 0; Mismatches 56; Indels 48; Gaps 4;

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 DB 128 TAAGGTCAGGTCGCGAGTTCGAATCTGCCAGACCCACCAATTTGCTGGGAAACGCC 187  
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 DB 488 CTTACAGTATAACCAAGATTCCTGGGTTATAT 521

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 DEFINITION complete sequence.  
 ACCESSION AF364307  
 VERSION AF364307.1 GI:13926168  
 KEYWORDS Pseudomonas tolaasii.  
 SOURCE Pseudomonas tolaasii.  
 ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.  
 REFERENCE 1 (bases 1 to 521)  
 AUTHORS Munsch, P. and Alatosava, T.  
 TITLE ITS 1 internal transcribed spacer  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 521)  
 AUTHORS Munsch, P. and Alatosava, T.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-MAR-2001) REDEC of Kajaani, Biotechnology Laboratory, University of Oulu, Salmelantie 43, Sotkamo 88600, Finland  
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BASE COUNT 136 a 107 c 130 g 148 t  
 ORIGIN determined"

Query Match 61.6%; Score 288.4; DB 1; Length 521;  
 Best Local Similarity 79.8%; Pred. No. 5.9e-71;  
 Matches 410; Conservative 0; Mismatches 56; Indels 48; Gaps 4;

QY 1 ATCGACGACATCAGCTGCTCATAAGCTCCACACGAATGCTTGATTCATTGAAGAAGA 60  
 DB 10 ATCGACGACATCAGCTGCTCATAAGCTCCACACGAATGCTTGATTCATTGAAGAAGA 69  
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 DB 488 CTTACAGTATAACCAAGATTCCTGGGTTATAT 521

RESULT 9  
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 DEFINITION sequence.  
 ACCESSION AF364308  
 VERSION AF364308.1 GI:13926169  
 KEYWORDS Pseudomonas tolaasii.  
 SOURCE Pseudomonas tolaasii.  
 ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.  
 REFERENCE 1 (bases 1 to 523)  
 AUTHORS Munsch, P. and Alatosava, T.  
 TITLE ITS 1 internal transcribed spacer  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 523)  
 AUTHORS Munsch, P. and Alatosava, T.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-MAR-2001) REDEC of Kajaani, Biotechnology Laboratory, University of Oulu, Salmelantie 43, Sotkamo 88600, Finland  
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Best Local Similarity 79.5%; Pred. No. 2.2e-70;
Matches 410; Conservative 0; Mismatches 56; Indels 50; Gaps 4;
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Db 70 CGATAAG--AAGCAGCCCGAAATTCGATGGTCTGTAGCTCAGTGGTGTAGAGCGCACCCCTGA 127
QY 121 TAAGGGTGAGGTGGGAGTTCGAATCTGCCAGACCCACCAATTTTGTCT----- 168
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Db 248 ACGGTTTCGATCCCGCTTGGCTCCACACCTACTGCTTCTAGCTTATGAACTTAGAAATG 307
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QY 328 AAAATTTGGTATGTATGATAAAGATAGCTGGACAGCACTTTCACCTGGTGTGTGTCAG 387
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Db 428 GCTAAGGTAAATTTGTGAGTTACTCAGTTTGTGATTTATCGAATTTTCGGCGAATGTT 487
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Db 488 GTCTTCACGATATAACAGATTCGTTGGGTTATAT 523
RESULT 10
AF127582 541 bp DNA linear BCT 10-MAR-2001
LOCUS
DEFINITION
Pseudomonas reactans strain H22 16S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, complete sequence;
tRNA-Ile and tRNA-Ala genes, complete sequence; and 23S ribosomal
RNA gene, partial sequence.
ACCESSION
AF127582
VERSION
AF127582.1 GI:13270380
KEYWORDS
Pseudomonas reactans.
SOURCE
Pseudomonas reactans.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE
1 (bases 1 to 541)
AUTHORS
Kwon, S.W. and Cheon, M.S.
TITLE
Direct Submission
JOURNAL
Submitted (11-FEB-1999) Division of Molecular Genetics, National
Institute of Agricultural Science and Technology, Seodun-dong 249,
Suwon, Kyunggi-do 441-707, Republic of Korea
FEATURES
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Best Local Similarity 79.4%; Pred. No. 4.8e-70;
Matches 408; Conservative 0; Mismatches 58; Indels 48; Gaps 4;
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Db 253 ACGGTTTCGATCCCGCTTGGCTCCACCACTACTGCTTCTGGTATGAAAGCTTAGAAATG 312
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RESULT 11
AF127580 541 bp DNA linear BCT 10-MAR-2001
LOCUS
DEFINITION
Pseudomonas reactans strain pf1 16S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, complete sequence;
tRNA-Ile and tRNA-Ala genes, complete sequence; and 23S ribosomal
RNA gene, partial sequence.
ACCESSION
AF127580
VERSION
AF127580.1 GI:13270378
KEYWORDS
Pseudomonas reactans.
SOURCE
Pseudomonas reactans.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
REFERENCE
1 (bases 1 to 541)
AUTHORS
Kwon, S.W. and Cheon, M.S.
TITLE
Direct Submission
JOURNAL
Submitted (11-FEB-1999) Division of Molecular Genetics, National
```

Institute of Agricultural Science and Technology, Seodun-dong 249,  
Suwon, Kyunggi-do 441-707, Republic of Korea

## FEATURES

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/strain="pf1"  
/db\_xref="taxon:117680"  
/note="(J.M. Wells)"  
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12..526  
/product="internal transcribed spacer 1"  
97..170  
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204..276  
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527..541  
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BASE COUNT 146 a 110 c 134 g 151 t  
ORIGIN

Query Match 60.6%; Score 283.6; DB 1; Length 541;  
Best Local Similarity 79.2%; Pred. No. 1.4e-69;  
Matches 407; Conservative 0; Mismatches 59; Indels 48; Gaps 4;

Qy 1 ATCGACGACATCAGCTGCTCATAGCTCCACACAGAAATGCTTGATTCATTGAAGAAGA 60  
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Qy 61 CGATTAGGTTAGCAACCTTCGATGGGCTGTAGCTAGCTAGGTTAGAGCGACCCCTGA 120  
Db 75 CGATAAG--AAGCAGCCGCGAAATGGGCTGTAGCTAGCTAGGTTAGAGCGACCCCTGA 132  
Qy 121 TAAGGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAATTT-----165  
Db 133 TAAGGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAATTTTGTGGGAACGCC 192  
Qy 166 -----GCTGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCCTTGCACGAGGAGTCA 217  
Db 193 TGTAGAAATATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCCTTGCACGAGGAGTCA 252  
Qy 218 GCGGTTCCGATCCCGTTGGCTCCACACCGCCGCTGGCCAGTTGTCAGGTTGAAGCTTGA 277  
Db 253 ACGGTTCGATCCCGTTGGCTCCACACCGCTGGCTTGTGCTTATGAAGCTTGAAGATG 312  
Qy 278 AATATTC-----CGCTCGAATATGATTTCTGAACCTTATCAGAACTGCTTTTA 327  
Db 313 AGCATTCATCAAGATGATGATGTTGATTTCTAGTCTTTGATAGATCGTTCTTTA 372  
Qy 328 AAAATTTGGGTATGTGATAGAAAGATAGCTGGACAGACCTTCACTGGTGTGTTTCAAG 387  
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Qy 388 GCTAAGTAAATTTGTGAGT-----AATTACAAGTTTTCGGCGAATGTTGT 434  
Db 433 GCTAAGTAAATTTGTGAGTCTCTTAATTGAGAAATTCGAATTTTCGGCGAATGCTGT 492  
Qy 435 CTTACAGTATAACAGATGCTTTGGGGTTATAT 468  
Db 493 CTTACAGTATAACAGATGCTTTGGGGTTATAT 526

RESULT 12  
AF127590

LOCUS

DEFINITION

Accession

Version

Keywords

Source

AF127590 543 bp DNA linear BCT 10-MAR-2001  
Pseudomonas reactans strain ATCC14340 16S ribosomal RNA gene,  
partial sequence; internal transcribed spacer 1, complete sequence;  
rRNA-1le and rRNA-Ala genes, complete sequence; and 23S ribosomal  
RNA gene, partial sequence.

AF127590  
AF127590.1 GI:13270388  
Pseudomonas reactans.

## ORGANISM

Pseudomonas reactans  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.

## REFERENCE

1 (bases 1 to 543)  
Kwon,S.W. and Cheon,M.S.  
Direct Submission

## TITLE

Submitted (11-FEB-1999) Division of Molecular Genetics, National  
Institute of Agricultural Science and Technology, Seodun-dong 249,  
Suwon, Kyunggi-do 441-707, Republic of Korea

## JOURNAL

Location/Qualifiers

## FEATURES

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/strain="ATCC14340"

/db\_xref="ATCC:14340"

/db\_xref="taxon:117680"

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/product="internal transcribed spacer 1"

97..170

/product="rRNA-1le"

204..276

/product="rRNA-Ala"

529..543

/product="23S ribosomal RNA"

BASE COUNT 147 a 109 c 133 g 154 t

ORIGIN

Query Match 59.5%; Score 278.4; DB 1; Length 543;  
Best Local Similarity 78.5%; Pred. No. 4.1e-68;

Matches 405; Conservative 0; Mismatches 61; Indels 50; Gaps 4;

Qy 1 ATCGACGACATCAGCTGCTCATAGCTCCACACAGAAATGCTTGATTCATTGAAGAAGA 60  
Db 15 ATCGACGACATCAGCTGCTCATAGCTCCACACAGAAATGCTTGATTCATTGAAGAAGA 74  
Qy 61 CGATTAGGTTAGCAACCTTCGATGGGCTGTAGCTAGCTAGGTTAGAGCGACCCCTGA 120  
Db 75 CGATAA--CAAGCAGCCGCGAAATGGGCTGTAGCTAGCTAGGTTAGAGCGACCCCTGA 132  
Qy 121 TAAGGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAATTTTGTGGGAACGCC 165  
Db 133 TAAGGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAATTTTGTGGGAACGCC 192  
Qy 166 -----GCTGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCCTTGCACGAGGAGTCA 217  
Db 193 TGTAGAAATATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCCCTTGCACGAGGAGTCA 252  
Qy 218 GCGGTTCCGATCCCGTTGGCTCCACACCGCCGCTGGCCAGTTGTCAGGTTGAAGCTTGA 277  
Db 253 ACGGTTCGATCCCGTTGGCTCCACACCGCTGGCTTGTGCTTATGAAGCTTGAAGATG 312  
Qy 278 AATATTC-----CGCTCGAATATGATTTCTGAACCTTATCAGAACTGCTTTTA 327  
Db 313 AGCATTCATCAAAATGATGATGTTGATTTCTAGTCTTTGATAGATCGTTCTTTA 372  
Qy 328 AAAATTTGGGTATGTGATAGAAAGATAGCTGGACAGACCTTCACTGGTGTGTTTCAAG 387  
Db 373 AAAATTTGGGTATGTGATAGAAAGATAGCTGAACCTTCACTGGTGAACGATCAG 432  
Qy 388 GCTAAGTAAATTTGTGAGT-----TGAGTAATACAAAGTTTTCGGCGAATGTT 432  
Db 433 GCTAAGTAAATTTGTGAGTTACTCAGTTTGTAGTATTCGAATTTTCGGCGAATGTT 492  
Qy 433 GCTCTCAGTATAACAGATGCTTTGGGGTTATAT 468  
Db 493 GCTCTCAGTATAACAGATGCTTTGGGGTTATAT 528

RESULT 13

AF127585

LOCUS

DEFINITION

Accession

Version

Keywords

Source

AF127585 526 bp DNA linear BCT 10-MAR-2001  
Pseudomonas fluorescens strain LMG5939 16S ribosomal RNA gene,

partial sequence; internal transcribed spacer 1, complete sequence;  
trna-ile and trna-ala genes, complete sequence; and 23S ribosomal  
RNA gene, partial sequence.

ACCESSION AF127585.1 GI:13270383  
VERSION AF127585  
KEYWORDS Pseudomonas fluorescens.  
SOURCE Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
ORGANISM Pseudomonas.

REFERENCE 1 (bases 1 to 526)  
AUTHORS Kwon,S.W. and Cheon,M.S.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-1999) Division of Molecular Genetics, National  
Institute of Agricultural Science and Technology, Seodun-dong 249,  
Suwon, Kyunggi-do 441-707, Republic of Korea

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97..168  
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202..274  
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512..526  
/product="23S ribosomal RNA"  
136 a 108 c 135 g 147 t

rRNA  
misc\_RNA  
trRNA  
trRNA  
rRNA  
BASE COUNT 136 a 108 c 135 g 147 t  
ORIGIN

Query Match 59.3%; Score 277.6; DB 1; Length 526;  
Best Local Similarity 81.5%; Pred. No. 6.9e-68;  
Matches 409; Conservative 0; Mismatches 54; Indels 39; Gaps 6;

QY 1 ATCGACGACATCAGTGTCTCATAAGCTCCACACGAAATTCGTTGATTCATTGAAGAAGA 60  
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Db 15 ATCGACGACATCAGTGTCTCATAAGCTCCACACGAAATTCGTTGATTCATTGAAGAAGA 74

QY 61 CGATTAGGTTAGCAACCTTCGATTGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGA 120  
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Db 75 CGATAAG--AAGCAGCCGAAATTTGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGA 132

QY 121 TAAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGCT----- 168  
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Db 133 TAA--GTGAGGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGCTGGGAAAGGCC 190

QY 169 -----GGGGCCATAGCTCAGCTGGGAGAGCGCTTGCACGAGGAGTCA 217  
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Db 191 TGTAGAAATACGGGGCCATAGCTCAGCTGGGAGAGCGCTTGCACGAGGAGTCA 250

QY 218 GCGTTTCGATCCGCTGGCTCCACACCCGCTTGCACGTTTGTCAAAGCTTAGAATG 277  
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Db 251 ACGGTTCGATCCGCTGGCTCCACCACTACTGCTTCTGTTGTTGAAGCTTAGAATG 310

QY 278 AATATT-----CGCTCGAATATTGATTTCTGACATTTTATCAGAACTGTTTAA 328  
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QY 329 AATATTTGGGTATGTAGAAAGATAGACTGGACAGCACTTTCACCTGGTGTGTTTCAGG 388  
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QY 389 CTAGGTAATTTTGTGAG--TAATTAACAAGTTTTCGGCGAAATGTTGCTTTCACAGTATA 446  
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QY 447 ACCAGATTGCTGGGGTTATAT 468  
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Db 490 ACCAGATTGCTGGGGTTATAT 511

RESULT 14  
AF127581  
LOCUS  
DEFINITION Pseudomonas reactans strain H3 16S ribosomal RNA gene, partial  
sequence; internal transcribed spacer 1, complete sequence;  
trna-ile and trna-ala genes, complete sequence; and 23S ribosomal  
RNA gene, partial sequence.

ACCESSION AF127581  
VERSION AF127581.1 GI:13270379  
KEYWORDS Pseudomonas reactans.  
SOURCE Pseudomonas reactans  
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.

REFERENCE 1 (bases 1 to 540)  
AUTHORS Kwon,S.W. and Cheon,M.S.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-1999) Division of Molecular Genetics, National  
Institute of Agricultural Science and Technology, Seodun-dong 249,  
Suwon, Kyunggi-do 441-707, Republic of Korea

FEATURES  
source  
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/organism="Pseudomonas reactans"  
/strain="H3"  
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/note="(J.M. Wells)"  
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12..525  
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97..170  
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204..275  
/product="trna-ala"  
526..540  
/product="23S ribosomal RNA"  
144 a 109 c 137 g 150 t

rRNA  
misc\_RNA  
trRNA  
trRNA  
rRNA  
BASE COUNT 144 a 109 c 137 g 150 t  
ORIGIN

Query Match 59.1%; Score 276.4; DB 1; Length 540;  
Best Local Similarity 79.8%; Pred. No. 1.5e-67;  
Matches 409; Conservative 0; Mismatches 56; Indels 49; Gaps 5;

QY 1 ATCGACGACATCAGTGTCTCATAAGCTCCACACGAAATTCGTTGATTCATTGAAGAAGA 60  
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Db 15 ATCGACGACATCAGTGTCTCATAAGCTCCACACGAAATTCGTTGATTCATTGAAGAAGA 74  
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QY 61 CGATTAGGTTAGCAACCTTCGATTGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGA 120  
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Db 75 CGATAAG--AAGCAGCCGAAATTTGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGA 132  
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QY 121 TAAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTT----- 165  
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Db 133 TAAGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTTGTGTTGGGAAAGGCC 192  
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QY 166 -----GCTGGGGCCATAGCTCAGCTGGGAGAGCGCTTGCACGAGGAGTCA 217  
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QY 218 GCGTTTCGATCCGCTGGCTCCACACCCGCTTGCAGTTTGTCAAAGCTTAGAATG 277  
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QY 278 AATATT-----CGCTCGAATATTGATTTCTGAACTTTATCAGAACTGTTCTTTA 327  
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Db 312 AGCAATTCATCGTGATGTGAATGTTGATTTCTAGTCTTGTATGATCGTTCTTTA 371  
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QY 328 AATATTTGGGTATGTAGAAAGATAGACTGGACAGCACTTTCACCTGGTGTGTTTCAG 387  
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QY 388 GCTAAGTAAATTTGTGAGT-----AATTACAAGTTTTCGCGGAATGTTGT 434  
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RESULT 15  
AF197570  
LOCUS  
DEFINITION  
Alcanivorax borkumensis strain LE4 16S ribosomal RNA gene, partial  
sequence; internal transcribed spacer 1, complete sequence;  
trRNA-Ile and trRNA-Ala genes, complete sequence; and 23S ribosomal  
RNA gene, partial sequence.

ACCESSION  
AF197570  
VERSION  
AF197570.1 GI:11640606  
KEYWORDS  
Alcanivorax borkumensis.  
SOURCE  
Alcanivorax borkumensis.  
ORGANISM  
Alcanivorax borkumensis.  
Bacteria; Proteobacteria; gamma subdivision;  
Alcanivorax/Fundibacter group; Alcanivorax.  
REFERENCE  
1 (bases 1 to 584)  
Wang, W.F. and Tan, H.M.  
Sequencing of 16S-23S ISR of rRNA from Alcanivorax borkumensis LE4  
Unpublished  
2 (bases 1 to 584)  
Wang, W.F. and Tan, H.M.  
Direct Submission  
TITLE  
Submitted (21-OCT-1999) Department of Microbiology, National  
University of Singapore, 10 Kent Ridge Crescent, Singapore 119260,  
Singapore

FEATURES  
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148..221  
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Best Local Similarity 78.3%; Pred No. 2.3e-67;  
Matches 403; Conservative 0; Mismatches 62; Indels 50; Gaps 4;

QY 1 ATCGACGACATCAGTGTCTCATAAGCTCCACAGAAATGCTTGCATTCAAGAAGA 60  
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Db 67 ATCGACGACATCAGTGTCTCATAAGTCCACAGAAATGCTTGCATTCAAGAAGA 126  
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QY 61 CGATTAGTTAGCAACCTTCGATGGGTCTGTAGCTAGTTGGTTAGAGCGACCCCTGA 120  
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QY 121 TAAGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAATTTGCT----- 168  
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Db 184 TAAGGTGAGGTGCGGAGTTCGAATCTGCCAGACCCACCAATTTGCTGGGAAACGCC 243  
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QY 169 -----GGGGCCATAGCTACGCTGGGAGAGCGGCTGCTTGCACGAGGAGTCA 217  
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Db 244 TGTAGAAATACGGGCCATAGCTCACTAAGTGGGAGAGCGCTGCCCTGACGAGGAGTCA 303  
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QY 218 GCGGTTGATCCCGCTTGGCTCCACCCCGCTTGGCAGTTTGTCAAAGGCTAGAAATG 277  
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Search completed: February 1, 2003, 03:05:14  
Job time : 965.563 secs

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QY 278 AATATTC-----GCGTCAATATTTGATTTCTGAACCTTATCAGAATCGTCTTTA 327  
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Db 364 AGCATTCATCAATCCGATGGTGAATTTGATTTCTAGTCTTTGACTAGTTCTGTTCTTTA 423  
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Db 424 AAAATTTGGGTATGTGATAGAAAAGATAGACTGAAACGTTACTTTTCACTGGTAAACGATCAC 483  
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QY 388 GCTAAGGTAAATTTG-----TGAGTAATTACAAGTTTTCGCGGAATGTTG 433  
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PF 13-JAN-2000; 2000JP-0004160.

XX

XX  
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PN W09600298-A1.
XX 04-JAN-1996.
XX 23-JUN-1995; 95WO-EP02452.
XX 07-APR-1995; 95EP-0870032.
XX 24-JUN-1994; 94EP-0870106.
XX (INNO-) INNOGENETICS NV.
XX Jannes G, Rossau R, Van Heuverswyn H;
XX WPI; 1996-068882/07.
XX Novel hybridisation assay for the detection of eubacteria - esp
XX Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX Claim 2; Fig 36; 248pp; English.
XX The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
XX regions derived from various microorganisms. These sequences were
XX used in the method of the invention for the detection and identification
XX of at least one or more microorganisms. The method comprises amplifying
XX the 16S-23S rRNA spacer region and hybridising one or more of the probes
XX given in AAT34011-77 to the amplified sequence. These probes were
XX specifically used to detect microorganisms in samples originating from
XX the respiratory tract. This spacer region is derived from Pseudomonas
XX aeruginosa U2G 5669.
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XX Query Match 46.28; Score 216; DB 17; Length 471;
XX Best Local Similarity 74.98; Pred. No. 6e-59;
XX Matches 370; Conservative 0; Mismatches 75; Indels 49; Gaps 6;
XX
XX QY 1 ATCGACGACATGCTGTCTCATAGCTCCACACGAGTTCCTGATTCATTGAAGAAGA 60
XX Db 1 ATCGAAGATCCCGCTCTTCTCATAGCTCCACACGAGTTCCTGATTCATTGAAGA 59
XX
XX QY 61 CGATTAGGTAGCAACCTTCGATTGGGTCTGTAGCTCAGTTGGTTAGAGCCACCCCTGA 120
XX Db 60 -----CGATTGGGTCTGTAGCTCAGTTGGTTAGAGCCACCCCTGA 100
XX
XX QY 121 TAAGGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTT-----164
XX Db 101 TAAGGGTGAGTGGCGAGTTCGAATCTGCCAGACCCACCAATTTGGTGTGCTGCTG 160
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XX QY 165 -----TCTGGGGCCATGCTAGCTGGGAGCGCCTGCTTGCACGAGGAGTGCAGC 219
XX Db 161 ATCGATACGGGGCCATGCTAGCTGAGGAGCGCCTGCTTGCACGAGGAGTGCAGG 220
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XX QY 220 GGTTCGATCCCGTTGCTCCACACCCGCTTCCAGTTTGTCAAAGCTTAGAAATGAA 279
XX Db 221 AGTTCGATCTCTTGGCTCCACCATC---TAAACCAATCTGCGAAGCTCAGAAATGAA 277
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XX QY 280 TATTCG-CGTGCAATATTGATTCTTGAACCTTT--ATCAGAAATCTGCTTTAAATAATTGG 336
XX Db 278 TGTTCTGGGATGAACATTTGATTTCTGCTTTGCACCAAGACTGCTTTAAATAATTGG 337
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XX QY 337 GTATGATAGAAAGATAGACTGGACAGCACTTTCCTACTGTGTGTGTCTAGGCTAAGGTA 396
XX Db 338 GTATGATAGAAAGATAGACTGAATGATCTCTTTTCACTGTGTATCAAGTCAAGGTA 397
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XX QY 397 AAATTTGTGAGT--AATTACAAAGTTTTCGGCGAATGTTGCTTCACAGTATACCAAGTT 454
XX Db 398 AAATTTGCGAGTTCACCGCGAATTTTCGGCGAATGTTGCTTCACAGTATACCAAGTT 457
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XX QY 455 GCTTGGGGTTATAT 468
XX Db 458 GCTTGGGGTTATAT 471
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RESULT 4
AAT11844
ID AAT11844 standard; DNA; 504 BP.
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XX AC AAT11844;
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XX DT 03-SEP-1996 (first entry)
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XX DE P. stutzeri LMG 2333 16S-23S rRNA spacer region.
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XX KW Probe; detection; identification; microorganism; amplification;
XX KW 16S-23S rRNA spacer region; respiratory tract; universal;
XX KW species-specific; ss.
XX
XX OS Pseudomonas stutzeri.
XX
XX PN W09600298-A1.
XX
XX PD 04-JAN-1996.
XX
XX PF 23-JUN-1995; 95WO-EP02452.
XX
XX PR 07-APR-1995; 95EP-0870032.
XX PR 24-JUN-1994; 94EP-0870106.
XX
XX PA (INNO-) INNOGENETICS NV.
XX
XX PJ Jannes G, Rossau R, Van Heuverswyn H;
XX
XX DR WPI; 1996-068882/07.
XX
XX PT Novel hybridisation assay for the detection of eubacteria - esp
XX PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
XX PS Claim 2; Fig 38; 248pp; English.
XX
XX CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
XX CC regions derived from various microorganisms. These sequences were
XX CC used in the method of the invention for the detection and identification
XX CC of at least one or more microorganisms. The method comprises amplifying
XX CC the 16S-23S rRNA spacer region and hybridising one or more of the probes
XX CC given in AAT34011-77 to the amplified sequence. These probes were
XX CC specifically used to detect microorganisms in samples originating from
XX CC the respiratory tract. This spacer region is derived from Pseudomonas
XX CC stutzeri LMG 2333.
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XX SQ Sequence 504 BP; 119 A; 111 C; 137 G; 137 T; 0 other;
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XX Query Match 43.88; Score 205.2; DB 17; Length 504;
XX Best Local Similarity 74.78; Pred. No. 1.8e-55;
XX Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;
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XX QY 1 ATCGACGACATGCTGTCTCATAGCTCCACACGAGTTCCTGATTCATTGAAGAAGA 59
XX Db 1 ATCGAAGACACCGCTCTGCTCATAGCTCCACACGAGTTCCTGATTCATTGAAGAAGA 60
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XX QY 60 ACGATTAGTTAGCAACCTT-----CGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 113
XX Db 61 GCGATTGGGTTCAGACCCGAGAGTAACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120
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XX QY 114 CCCCTGATAAGGGTGAGTTCGGCAGTTCGAATCTGCCAGACCCACCAATTTGCTGGGGC 173
XX Db 121 CCCCTGATAGGGTGAGTTCGGCAGTTCGAATCTGCCAGACCCACCAATTTGCTGGGGC 179
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XX QY 174 CATAGCTCAGCTGGGAGAGCGCTTCCCTTGACGAGGAGTTCAGCGGTTTCGATCCCGCT 233
XX Db 180 CATAGCTCAGCTGGGAGAGCGCTTCCCTTGACGAGGAGTTCAGCGGTTTCGATCCCGCT 239
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XX QY 234 TGGCTCCACC-----ACCCCGCTTGGCAGTTTGTCAAAGCTTAGAA 274
XX Db 240 TGGCTCCACCATTAACTCTAGTCCCGGAAAGCTCAGAAATGAGTGTTCACGAGTATGAGG 299
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XX QY 275 ATGAATATTCGGTTCGAATATTGATTCTTGAACCTTT--ATCAGAAATCGTCTTTAAAAAT 332
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Db 300 TTGATGCGTGGTGAACATGATTTCTGGACTTGGCCAGAACTGTTCTTTAAAT 359
QY 333 TTGGTATGTGATGAAGAATAGATGGACAGCACTTTCACCTGGTGTGGTTCAGGCTAA 392
Db 360 TTGGGTATGTGATGAAGAATAGATGGACAGCACTTTCACCTGGTGTGGTTCAGGCTAA 418
QY 393 GGTAAATTTGAGTAAT--TACAAGTTTTCGGGGAATGTGCTTCACAGTA----- 444
Db 419 GGTAAATTTGCGTGTCTCTATGCAAAATTTTCGGGCAATGTCGTTCCACGTTATAGAC 478
QY 445 --TAACCAGATTGCTTGGGGTTATAT 468
Db 479 AGTAACCAGATTGCTTGGGGTTATAT 504

RESULT 5
AAT11845
ID AAT11845 standard; DNA; 499 BP.
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AC AAT11845;
XX
DT 03-SEP-1996 (first entry)
XX
DE P. alcaligenes LMG 1224 16S-23S rRNA spacer region.
XX
KW Probe; detection; identification; microorganism; amplify;
KW 16S-23S rRNA spacer region; respiratory tract; universal;
KW species-specific; ss.
XX
OS Pseudomonas alcaligenes.
XX
PN WO9600298-A1.
XX
PD 04-JAN-1996.
XX
PF 23-JUN-1995; 95WO-EF02452.
XX
PR 07-APR-1995; 95EP-0870032.
PR 24-JUN-1994; 94EP-0870106.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Jannes G, Rossau R, Van Heuverswyn H;
XX
WPI; 1996-068882/07.
XX
PT Novel hybridisation assay for the detection of eubacteria - esp
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
PS Claim 2; Fig 39; 248pp; English.
XX
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
CC regions derived from various microorganisms. These sequences were
CC used in the method of the invention for the detection and identification
CC of at least one or more microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes
CC given in AAT34011-77 to the amplified sequence. These probes were
CC specifically used to detect microorganisms in samples originating from
CC the respiratory tract. This spacer region is derived from Pseudomonas
CC alcaligenes LMG 1224.
XX
SQ Sequence 499 BP; 123 A; 109 C; 130 G; 137 T; 0 other;
Query Match 42.4%; Score 198.4; DB 17; Length 499;
Best Local Similarity 72.8%; Pred. No. 2.7e-53;
Matches 367; Conservative 0; Mismatches 96; Indels 41; Gaps 7;

QY 1 ATCGACGACATCAGCTGCTCTCAAGCTCCACACGAAATGCTTGAATTCATTGAAGAAGA 60
Db 1 ATCGAAGACTTCAGCTTCTTCATAAGTTCACACGAAATGCTTGAATTCAGTTCGGAAGA 60
QY 61 CGATTAGGTAGCAACCTT-----CGATTGGGTCTGTAGCTCAGTTCGTTAGACGCA 113

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Db 61 GCGATTGGGTTTCAGACCCGAGAGTACGATTCGGTCTGTAGCTCAGTTGTTAGACGCA 120
QY 114 CCCTCTGATAAGGTCGAGTCGCGAGTTCCGAATCTGCCAGAGCCACCAATTTGC----- 167
Db 121 CCCCTGATAAGGTCGAGTCGCGAGTTCCGAATCTGCCAGAGCCACCAATTTGTCGGGATG 180
QY 168 -----TGGGGCCATAGCTCAGCTGGGAGAGCCGCTGCTTCGACGAGGAGGT 215
Db 181 GCCAGTGTCAAAATGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTCGACGAGGAGGT 240
QY 216 CAGCGGTTTCGATCCCGCTTGGCTCCACACCCGCTTGGCAGTTTCTCAAGCTTAGAAA 275
Db 241 CAGGAGTTCGATCCCTCTTGGCTCCACCA--TCAACTCAGATCGCTGGAAGCTCAGAAA 298
QY 276 TGAATATTTCG-CGTGGAATATTGATTTCTGAACCTTT--ATCAGAATCGTTCTTTAAAT 332
Db 299 TGAACATTTGGTAGTTCATGTTGATTTCTGCTTTGGCCGACAGACTGTTCTTTAAAT 358
QY 333 TTGGGTATGTGATGAAGAATAGACTGGACAGCACTTTCACCTGGTGTGGTTCAGGCTAA 392
Db 359 TTGGGTATGTGATGA--AGTGACTAACAGCGTGTTCACCTGCACGTTGTTTAACAAG 415
QY 393 GGTAAATTTGTCAGTAATTAACAAGTTTCGGGGAATGTGTTCTTCAC-----AGTA 444
Db 416 CAAATTTGCGAGTTCAAGCGCAATTTTCGGGCAATGTCGTTTCACGTTACGAATCTA 475
QY 445 TAACCAGATTGCTTGGGGTTATAT 468
Db 476 TAACCAGATTGCTTGGGGTTATAT 499

RESULT 6
AAT11843
ID AAT11843 standard; DNA; 520 BP.
XX
AC AAT11843;
XX
DT 03-SEP-1996 (first entry)
XX
DE P. pseudoalcaligenes LMG 1225 16S-23S rRNA spacer region.
XX
KW Probe; detection; identification; microorganism; amplify;
KW 16S-23S rRNA spacer region; respiratory tract; universal;
KW species-specific; ss.
XX
OS Pseudomonas pseudoalcaligenes.
XX
PN WO9600298-A1.
XX
PD 04-JAN-1996.
XX
PF 23-JUN-1995; 95WO-EF02452.
XX
PR 07-APR-1995; 95EP-0870032.
PR 24-JUN-1994; 94EP-0870106.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Jannes G, Rossau R, Van Heuverswyn H;
XX
WPI; 1996-068882/07.
XX
PT Novel hybridisation assay for the detection of eubacteria - esp
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region
XX
PS Claim 2; Fig 37; 248pp; English.
XX
CC The sequences given in AAT11791-857 represent the 16S-23S rRNA spacer
CC regions derived from various microorganisms. These sequences were
CC used in the method of the invention for the detection and identification
CC of at least one or more microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes
CC specifically used to detect microorganisms. The method comprises amplifying
CC the 16S-23S rRNA spacer region and hybridising one or more of the probes

```

CC given in AAT34011-77 to the amplified sequence. These probes were  
 CC specifically used to detect microorganisms in samples originating from  
 CC the respiratory tract. This spacer region is derived from *Pseudomonas*  
 CC *pseudoalcaligenes* LMG 1225.

XX Sequence 520 BP; 126 A; 109 C; 134 G; 151 T; 0 other;  
 SQ  
 Query Match 38.0%; Score 178; DB 17; Length 520;  
 Best Local Similarity 71.1%; Pred. No. 9.8e-47;  
 Matches 371; Conservative 0; Mismatches 95; Indels 56; Gaps 8;  
 QY 1 ATCGACGACATCAGCTGCTCATAAGCTCCACACGAATGCTGATTCATTGAGAAGA 60  
 DB 1 ATCGAAGACATCAGCTTCTCATAGTATCCACACGAATGCTGATTCATTGAGAAGA 60  
 QY 61 CGATTAGGTAGCACACTTCGAT-TGGGTCCTAGCTAGTGGTGTAGAGCCACCCCTG 119  
 DB 61 AATGCTGTAAACGACCGCTGTTATAGTCTGTAGTCTAGTGGTGTAGAGCCACCCCTG 120  
 QY 120 ATAAGGTTGAGTGGCAGTTCGAATCTGCCAGACCCACCAATTTGCT----- 168  
 DB 121 ATAAAGGTTGAGTGGCAGTTCGAATCTGCCAGACCCACCAATTTGCT----- 168  
 QY 169 -----GGGCCATAGCTAGCTGGGAGAGCGCTGCTTGCAGCAGGAGGTGAGCGGTTTC 224  
 DB 181 ATACGGGGCCATAGCTAGCTGGGAGAGCGCTGCTTGCAGCAGGAGGTGAGCGGTTTC 240  
 QY 225 GATCCCGCTTGGCTCCACACCC-----CGCTTGCAGTGTGCAAGCTTAGAATG 277  
 DB 241 GATCCCGCTTGGCTCCACACCTCTCGTGTGCGGTGAGTGTAAAGAGTTTCAGAAATG 300  
 QY 278 A-----ATATTCGGCTCGAATATTGATTTCTGAACTT-----TATCAGAA 317  
 DB 301 ATGCGGCTTACGTTTGCCTGTTGAGTCTGCTGATTTCTGGCTTTTGACCGGTACGAAA 360  
 QY 318 TCGTCTTTAAATTTGGGTATGTATGATAGAAAGATAGACTGGACGACCTTTCACTGGT 377  
 DB 361 TCGTCTTTAAATTTGGGTATGTATGATAGAAAGATAGACTGATTAATG--CTTCACTGGC 418  
 QY 378 GTGTCTCAGCTTAAGTAAATTTGTGAGT---AATTACAAGTTTTCGGCGAATGTTG 433  
 DB 419 AATTGATCTGCTCAAGTAAATTTGTGAGTCTCAAGACGCAATTTTCGGCGAATGTCG 478  
 QY 434 TCTTCAC-----AGTAAACCAAGATTGCTTGGGGTTATAT 468  
 DB 479 TCTTCACGATTGACAGACAGTAAACCAAGATTGCTTGGGGTTATAT 520

## RESULT 7

ABA92787  
 ID ABA92787 standard; DNA; 640681 BP.

XX ABA92787;  
 AC

XX 27-MAR-2002 (first entry)  
 DT

XX Buchnera sp. genomic DNA SEQ ID NO:1.  
 XX

XX Buchnera; cockroach-symbiotic bacterium; cockroach extermination;  
 KW circular; ds.  
 KW

XX Buchnera sp.  
 OS

XX JF2001292771-A.  
 PN

XX 23-OCT-2001.  
 PD

XX 07-APR-2000; 2000JP-0107160.  
 PF

XX 07-APR-2000; 2000JP-0107160.  
 PR

XX (RIKA ) RIKAGAKU KENKYUSHO.  
 PA

XX

DR WPI; 2002-126043/17.

XX A genomic DNA of cockroach-symbiotic bacterium -  
 PT

PS Claim 1; Page 16-230; 237pp; Japanese.  
 XX

CC The present invention describes a gene (I) derived from *Buchnera* sp.  
 CC containing the DNA (a) or (b), (a) has a fully defined base pair  
 CC sequence selected from a table of sequences found in the *Buchnera* sp.  
 CC genomic DNA of ABA92787 given in the specification or is a DNA selected  
 CC from complementary DNA sequences, and (b) is a DNA which hybridises with  
 CC the DNA (a) and encodes a protein. Also described are: (1) a recombinant  
 CC vector (II) containing (1); (2) a transformant (III) containing (II);  
 CC (3) a genomic DNA of *Buchnera* sp. containing the sequence given in  
 CC ABA92787; (4) a plasmid derived from *Buchnera* sp. containing DNA (c) or  
 CC or ABB92789 and (d) is a plasmid which hybridises with a DNA; and (5) a  
 CC method for the preparation of a protein in which (III) is cultured and  
 CC the expression protein of the objective protein is collected from the  
 CC resultant culture. The DNA is useful for developing agricultural  
 CC chemicals for exterminating cockroaches. The present sequence represents  
 CC the specifically claimed *Buchnera* sp. genomic DNA sequence, from the  
 CC present invention.

SQ Sequence 640681 BP; 237522 A; 83822 C; 84757 G; 234580 T; 0 other;

Query Match 23.7%; Score 110.8; DB 24; Length 640681;  
 Best Local Similarity 79.0%; Pred. No. 1.3e-23;  
 Matches 147; Conservative 0; Mismatches 32; Indels 7; Gaps 1;

QY 63 ATTAGGTAGCAACCTTCGATGGGTCTGTAGCTAGTGGTGTAGAGCGACCCCTGATA 122  
 DB 275618 ATTATCTATAAATAAATAATAGAGGCTTGTAGCTCAGATGGTGTAGAGCGACCCCTGATA 122

QY 123 AGGGTGAGGTGCGGCGAGTTCGAATCTGCCAGACCCACCC-----AATTTGCTGGGGCCA 175  
 DB 275678 AGGGTGAGGTGCGGTTCAATTCACCTCAGGCTACCAATAAATAATCATCTGGGGCTA 275737

QY 176 TAGCTCAGCTGGGAGAGCGCCCTGCTTGCACGAGAGGTGACGGTTCGATCCCGCTTG 235  
 DB 275738 TAGCTCAGCTGGGAGAGCGCCCTGCTTGCACGAGAGGTGACGGTTCGATCCCGCTTG 235

QY 236 GCTCCA 241  
 DB 275798 GCTCCA 275803

## RESULT 8

AAQ14102  
 ID AAQ14102 standard; DNA; 603 BP.

XX AAQ14102;  
 AC

XX 10-JAN-1992 (first entry)  
 DT

XX *N.gonorrhoeae* strain NCTC 8375 16S to 23S rRNA gene spacer region.  
 DE

XX rRNA gene; ribosomal RNA; probe; ss.  
 KW

XX *Neisseria gonorrhoeae* NCTC 8375.  
 OS

XX EP452596-A.  
 PN

XX 23-OCT-1991.  
 PD

XX 18-APR-1990; 90EP-0401054.  
 PF

XX 18-APR-1990; 90EP-0401054.  
 PR

XX (INNO-) INNOGENETICS NV SA.  
 PA

XX Rossau R, Van Heuverswijn H;  
 PI

XX

DR WPI; 1991-311940/43.  
XX Hybridisation probes for detecting non-viral microorganisms -  
PT derived from spacer region between 16S and 23S rRNA genes, for  
PT detecting e.g. BORDETELLA PERTUSSIS, NEISSERIA GONORRHOEA  
XX  
XX Disclosure; Fig 3; 41pp; English.  
XX  
XX This sequence is the non-coding strand of the 16S-23S rRNA gene  
CC spacer region; the 5'-end is proximal to the 16S rRNA gene and the 3'  
CC -end proximal to the 23S rRNA gene. The sequence is very similar  
CC to the corresponding region in N.gonorrhoeae ITM 4367. A set of  
CC probes was designed based on this sequence which was specific for  
CC N.gonorrhoeae. A kit is provided for detection of N.gonorrhoeae  
CC using the probes.  
XX  
SQ Sequence 603 BP; 203 A; 104 C; 145 G; 151 T; 0 other;  
Query Match 23.3%; Score 109; DB 12; Length 603;  
Best Local Similarity 62.5%; Pred. No. 1.4e-24;  
Matches 167; Conservative 0; Mismatches 110; Indels 2; Gaps 1;  
QY 85 GGGTCTGTACCTCAGTGTGTAGAGCGCACCCCTGATAGAGGTGAGTGGCGAGTTCGAA 144  
DB 99 GGGTCTGTAGCTCAGCTGGTGTAGAGCACACGCTTGATAGCGGTGAGGTGCGAGGTCAAG 158  
QY 145 TCTGCCAGACCCACCAATTTGCTGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCCCTTC 204  
DB 159 TCTCCAGACCCACCAA--GACGGGGGATAGCTCAGTGTGTAGAGCACCTGCTTTC 216  
QY 205 ACGCAGGAGTGCAGCGTTCGATCCCGCTTGGCTCCACCCACCCGCTTGCCAGTTTGCA 264  
DB 217 AAGCAGGGGCTCATCGTTCGATCCCGCTTGGCTCCACCAAACTTTTACAAATGAAAGCA 276  
QY 265 AAGCTTAGAATGAATATTCGCGTCGATATTTGATTTCGAAAGTAGAATAACGACGCATCGATCT 324  
DB 277 AGTTTGTGTTTTAGCAGCTTATTTTGTATTTGCGAAGTAGAATAACGACGCATCGATCT 336  
QY 325 TTAATAATTTGGGTATGTATGATAGAAATAGACTGGACACACTTTTCACTGGTGTGTGT 383  
DB 337 TTACAAATTTGGAAGCGGAATACACAAACAAAGACAATGAGTTGTTTGTATTTTTT 395  
RESULT 9  
ID AAV78022 standard; DNA; 400 BP.  
XX AAV78022;  
XX  
XX 16-MAR-1999 (first entry)  
XX Staphylococcus aureus contig SEQ ID #3711.  
XX  
XX Computer readable medium; vaccine; S.aureus infection; immunodetection;  
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
KW skin infection; surgical wound infection; scalded skin syndrome;  
KW toxic shock syndrome; ds.  
XX  
XX Staphylococcus aureus.  
XX  
XX EP786519-A2.  
XX  
XX 30-JUL-1997.  
XX  
XX 07-JAN-1997; 97EP-0100117.  
XX  
XX 05-JAN-1996; 96US-0009861.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Barash, SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;  
PI Rosen CA;  
XX

DR WPI; 1997-374922/35.  
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
PT stored on computer readable medium and used in the production of  
PT anti-S.aureus vaccines  
XX  
XX Claim 1; Page 2654; 3271pp; English.  
XX  
XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
CC of the invention. The DNA sequences are recorded on a computer readable  
CC medium, preferably selected from a floppy or hard disk, random access  
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
CC the S.aureus DNA sequences allows putative functions to be assigned so  
CC that protein-encoding or regulatory regions of commercial, therapeutic or  
CC industrial importance can be obtained. Specifically, sequences which are  
CC likely to encode antigens have been identified and these polypeptides can  
CC be used in a vaccine composition against S.aureus infection. The  
CC polypeptides can also be used in a kit for the immunodetection of  
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
CC for recombinant production of the polypeptides. The new DNA sequences  
CC (and their fragments) are useful as primers or probes for isolating  
CC homologues of any of the S.aureus DNA sequences contained on the  
CC computer readable medium.  
XX  
SQ Sequence 400 BP; 104 A; 79 C; 104 G; 113 T; 0 other;  
Query Match 22.5%; Score 105.2; DB 18; Length 400;  
Best Local Similarity 67.9%; Pred. No. 1.9e-23;  
Matches 167; Conservative 0; Mismatches 68; Indels 11; Gaps 1;  
QY 10 ATCAGCTGTCTCATAGCTCCACACGAATTCCTTGTATTCATTGAAGAAGACGATTAGGT 69  
DB 115 AACATCTCTTCAGAAATGCGGAATACGTGACATATGTATTTCAGTTTGAATGTTTG 174  
QY 70 TAGCAACCTTCGATGGTGTGTAGTCTAGTGTGTGTAGAGCGCACCCCTGTATAGGGTGA 129  
DB 175 TTCATTCAAAATTAATGGGCTTATAGTCTAGCTGTGTAGAGCGCACCCCTGTATAGCGTGA 234  
QY 130 GGTGGCAGTTCGAATCTGCCACACCCCAAT-----TTGCTGGGGCCATAG 178  
DB 235 GGTGGTGGTTCGAGTCCACTTAGGCCACCACTTAATTAATACCTATTTCGGGGCTTAG 294  
QY 179 CTCAGCTGGGAGAGCGCTGCTTCACGACGAGGAGTCCAGCGGTTCGATCCCGCTGGCT 238  
DB 295 CTCAGCTGGGAGAGCGCTGCTTCGACGACGAGGAGTCCAGCGGTTCGATCCCGCTAGTCT 354  
QY 239 CCACCA 244  
DB 355 CCACCA 360  
RESULT 10  
ID AAV77902/c  
XX AAV77902 standard; DNA; 400 BP.  
XX AAV77902;  
XX  
XX 16-MAR-1999 (first entry)  
XX Staphylococcus aureus contig SEQ ID #3591.  
XX  
XX Computer readable medium; vaccine; S.aureus infection; immunodetection;  
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
KW skin infection; surgical wound infection; scalded skin syndrome;  
KW toxic shock syndrome; ds.  
XX  
XX Staphylococcus aureus.  
XX  
XX Key Location/Qualifiers  
XX misc\_feature 361..400  
XX  
XX



FT FT /\*tag= a  
 FT FT /note= "these bases represent a line of missing text in  
 FT FT the sequence listing in the specification. They  
 FT FT are included to maintain the nucleotide numbering  
 FT FT given in the specification for this DNA sequence"

EP786519-A2.

30-JUL-1997.

07-JAN-1997; 97EP-0100117.

05-JAN-1996; 96US-0009861.

(HUMA-) HUMAN GENOME SCI INC.

Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;

Rosen CA;

WPI; 1997-374922/35.

Polynucleotide(s) and proteins derived from *Staphylococcus aureus* -  
 stored on computer readable medium and used in the production of  
 anti-S.aureus vaccines

Claim 1; Page 2600; 3271pp; English.

This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences  
 of the invention. The DNA sequences are recorded on a computer readable  
 medium, preferably selected from a floppy or hard disk, random access  
 memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
 the S.aureus DNA sequences allows putative functions to be assigned so  
 that protein-encoding or regulatory regions of commercial, therapeutic or  
 industrial importance can be obtained. Specifically, sequences which are  
 likely to encode antigens have been identified and these polypeptides can  
 be used in a vaccine composition against S.aureus infection. The  
 polypeptides can also be used in a kit for the immunodetection of  
 S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
 including cellulitis, eyelid infections, scalded skin syndrome, toxic shock  
 syndrome, etc. Organisms transformed with the DNA sequences can be used  
 for recombinant production of the polypeptides. The new DNA sequences  
 (and their fragments) are useful as primers or probes for isolating  
 homologues of any of the S.aureus DNA sequences contained on the  
 computer readable medium.

Sequence 400 BP; 105 A; 82 C; 66 G; 107 T; 40 other;

Query Match 22.5%; Score 105.2; DB 18; Length 400;  
 Best Local Similarity 67.9%; Pred. No. 1.9e-23;  
 Matches 167; Conservative 0; Mismatches 68; Indels 11; Gaps 1;

QY 10 ATCAGCTGTCTCATAGCTCCACAGCAATTCCTTGATTCATTGAAGAGACGATTAGT 69

DB 348 ACATCTTCTTTCAGAAGATGCGGAATAACGTGCACATATTTGATTTCAGTTTGAATGTTG 289

QY 70 TAGCAACCTTCGATTGGTCTGTAGCTCAGTTGGTTAGAGCCACCCCTGATAAGGGTGA 129

DB 288 TTCAATCAAAATTAATGGGCTATACCTCAGCTGGTTAGAGCCACCCCTGATAAGCGTGA 229

QY 130 GGTGGGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178

DB 228 GGTGGTGGTTCGAGTCCACTTAGGCCACCAATTAATTAATTAATTAATTTGGGGCTTAG 169

QY 179 CTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTTCAGCGGTTCGATCCGCTTGGCT 238

DB 168 CTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTTCAGCGGTTCGATCCGCTTGGCT 109

QY 239 CCACCA 244

DB 108 CCACCA 103

RESULT 11

AAV77852

ID AAV77852 standard; DNA; 1311 BP.

XX AC AAV77852;

XX DT 16-MAR-1999 (first entry)

XX DE Staphylococcus aureus contig SEQ ID #3541.

XX KW Computer readable medium; vaccine; S.aureus infection; immunodetection;  
 XX KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
 XX KW skin infection; surgical wound infection; scalded skin syndrome;  
 XX KW toxic shock syndrome; ds.

XX OS Staphylococcus aureus.

XX PN EP786519-A2.

XX PD 30-JUL-1997.

XX PF 07-JAN-1997; 97EP-0100117.

XX PR 05-JAN-1996; 96US-0009861.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;

XX PI Rosen CA;

XX DR WPI; 1997-374922/35.

XX PT Polynucleotide(s) and proteins derived from *Staphylococcus aureus* -  
 stored on computer readable medium and used in the production of  
 anti-S.aureus vaccines

XX PS Claim 1; Page 2576; 3271pp; English.

XX CC This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences  
 of the invention. The DNA sequences are recorded on a computer readable  
 medium, preferably selected from a floppy or hard disk, random access  
 memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
 the S.aureus DNA sequences allows putative functions to be assigned so  
 that protein-encoding or regulatory regions of commercial, therapeutic or  
 industrial importance can be obtained. Specifically, sequences which are  
 likely to encode antigens have been identified and these polypeptides can  
 be used in a vaccine composition against S.aureus infection. The  
 polypeptides can also be used in a kit for the immunodetection of  
 S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
 including cellulitis, eyelid infections, scalded skin syndrome, toxic shock  
 syndrome, etc. Organisms transformed with the DNA sequences can be used  
 for recombinant production of the polypeptides. The new DNA sequences  
 (and their fragments) are useful as primers or probes for isolating  
 homologues of any of the S.aureus DNA sequences contained on the  
 computer readable medium.

Sequence 1311 BP; 380 A; 264 C; 328 G; 334 T; 5 other;

Query Match 22.5%; Score 105.2; DB 18; Length 1311;  
 Best Local Similarity 67.9%; Pred. No. 3.5e-23;  
 Matches 167; Conservative 0; Mismatches 68; Indels 11; Gaps 1;

QY 10 ATCAGCTGTCTCATAGCTCCACAGCAATTCCTTGATTCATTGAAGAGACGATTAGT 69

DB 590 AACATCTTCTTTCAGAAGATGCGGAATAACGTGCACATATTTGATTTCAGTTTGAATGTTG 649

QY 70 TAGCAACCTTCGATTGGTCTGTAGCTCAGTTGGTTAGAGCCACCCCTGATAAGGGTGA 129

DB 650 TTCAATCAAAATTAATGGGCTTATAGCTCAGCTGGTTAGAGCCACCCCTGATAAGCGTGA 709

QY 130 GGTGGGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178

Db 710 GGTGGTGGTTCAGTCCACTAGGCCACCATTAAATTAATACCTATTTGGGGCTTAG 769  
QY 179 CTGAGCTGGGAGCGCTGCTTGCACGAGGAGGTCAGCGTTCGATCCGCTTGGCT 238  
Db 770 CTGAGCTGGGAGCGCTGCTTGCACGAGGAGGTCAGCGTTCGATCCGCTAGTCT 829  
QY 239 CCACCA 244  
Db 830 CCACCA 835  
RESULT 12  
AAQ14106  
ID AAQ14106 standard; DNA: 664 BP.  
XX  
AC AAQ14106;  
XX  
DT 10-JAN-1992 (first entry)  
XX  
DE N.meningitidis NCTC 10025 16S to 23S rRNA gene spacer region.  
XX  
KW rRNA gene; ribosomal RNA; probe; ss.  
XX  
OS Neisseria meningitidis NCTC 10025.  
XX  
PN EP452596-A.  
XX  
PD 23-OCT-1991.  
XX  
PF 18-APR-1990; 90EP-0401054.  
XX  
PR 18-APR-1990; 90EP-0401054.  
XX  
PA (INNO-) INNOGENETICS NV SA.  
XX  
PI Rossau R, Van Heuverswijn H;  
XX  
DR WPI; 1991-311940/43.  
XX  
PT Hybridisation probes for detecting non-viral microorganisms -  
PT derived from spacer region between 16S and 23S rRNA genes, for  
PT detecting e.g. BORDETELLA PERTUSSIS, NEISSERIA GONORRHOEA  
XX  
PS Disclosure; Fig 3; 4lpp; English.  
XX  
CC This sequence is the non-coding strand of the 16S-23S rRNA gene  
CC spacer region; the 5'-end is proximal to the 16S rRNA gene and the 3'-  
CC -end proximal to the 23S rRNA gene. A set of probes was designed  
CC based on this sequence which was specific for N.meningitidis. A kit  
CC is provided for detection of this species using the probes.  
XX  
SQ Sequence 664 BP; 235 A; 123 C; 154 G; 152 T; 0 other;  
Query Match 22.4%; Score 104.8; DB 12; Length 664;  
Best Local Similarity 82.5%; Pred. No. 3.3e-23;  
Matches 132; Conservative 0; Mismatches 27; Indels 1; Gaps 1;  
QY 85 GGGTCTGTAGCTCAGTGGTTAGAGCGCACCCCTGATAAGGTTGAGTTCGAGTTCGAA 144  
Db 100 GGGTTGTAGTCTAGCTGTTAGAGCACACGCTTGATAGCGTGGGGTCTGGAGGTTCAAG 159  
QY 145 TCTGCCAGACCCACCAATTTGCTGGGCCATAGCTCAGCTGGGAGAGCGCTTGCCTTGC 204  
Db 160 TCTTCCAGAGACCCACCA- GAACGGGGGGCATAGCTCAGTTGGTAGAGCACCTGCTTGC 218  
QY 205 ACGCAGGAGGTCAGCGTTTCGATCCCGCTTGGCTCCACCA 244  
Db 219 AAGCAGGGGTCATCGGTTTCGATCCCGCTTGGCTCCACCA 258  
RESULT 13  
AAT11889  
ID AAT11889 standard; DNA: 808 BP.

XX  
AC AAT11889;  
XX  
DT 03-SEP-1996 (first entry)  
XX  
DE Brucella melitensis NIDO Biovar 1 16S-23S rRNA spacer region.  
XX  
KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; food; universal;  
KW species-specific; ss.  
XX  
OS Brucella melitensis.  
XX  
PN WO9600298-A1.  
XX  
PD 04-JAN-1996.  
XX  
PF 23-JUN-1995; 95WO-EP02452.  
XX  
PR 07-APR-1995; 95EP-0870032.  
PR 24-JUN-1994; 94EP-0870106.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Jannes G, Rossau R, Van Heuverswijn H;  
XX  
DR WPI; 1996-068882/07.  
XX  
PT Novel hybridisation assay for the detection of eubacteria - esp  
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
XX  
PS Claim 5; Fig 56; 248pp; English.  
XX  
CC The sequences given in AAT11889-905 represent the 16S-23S rRNA spacer  
CC regions derived from various microorganisms. These sequences were  
CC used in the method of the invention for the detection and identification  
CC of at least one or more microorganisms. The method comprises amplifying  
CC the 16S-23S rRNA spacer region and hybridising one or more probes to  
CC the amplified sequence. These probes were specifically used to detect  
CC microorganisms in samples originating from food. This spacer region is  
CC derived from Brucella melitensis NIDO Biovar 1.  
XX  
SQ Sequence 808 BP; 178 A; 181 C; 236 G; 211 T; 2 other;  
Query Match 22.3%; Score 104.4; DB 17; Length 808;  
Best Local Similarity 79.0%; Pred. No. 4.9e-23;  
Matches 139; Conservative 0; Mismatches 31; Indels 6; Gaps 1;  
QY 84 TGGTCTCTAGCTCAGTGGTTAGAGCGCACCCCTGATAAGGTTGAGTTCGAGTTCGA 143  
Db 279 TGGGCTTGTAGCTCAGTGGTTAGAGCACACGCTTGATAGCGTGGGGTTCGAGGTTCAA 338  
QY 144 ATCTGCCAGACCCACCAATTTGCT-----GGGCCATAGCTCAGCTGGGAGAGCGCT 197  
Db 339 GTCTTCCAGGCCACCAAGTTACTTGATGAGGGCCGTAGCTCAGCTGGGAGAGCACCT 398  
QY 198 GCCTTGCACGAGGAGTTCAGGGTTTCGATCCCGCTTGGCTCCACCCCGCTTG 253  
Db 399 GCTTGTGAAGCAGGGGGTTCGCTGCTGATCCCGCTCCGCTCCACCATCATGTTGG 454  
RESULT 14  
AAT11890  
ID AAT11890 standard; DNA: 808 BP.  
XX  
AC AAT11890;  
XX  
DT 03-SEP-1996 (first entry)  
XX  
DE Brucella suis NIDO Biovar 1 16S-23S rRNA spacer region.  
XX  
KW Probe; detection; identification; microorganism; amplify;  
KW 16S-23S rRNA spacer region; food; universal;

species-specific; ss.

KW

XX OS Brucella suis.

XX

PN WO9600298-A1.

XX

PD 04-JAN-1996.

XX

XX 23-JUN-1995; 95WO-EP02452.

XX

PF 07-APR-1995; 95EP-0870032.

XX

PR 24-JUN-1994; 94EP-0870106.

XX

XX (INNO-) INNOGENETICS NV.

XX

PI Jannes G, Rossau R, Van Heuverswyn H;

XX

DR WPI; 1996-068882/07.

XX

XX Novel hybridisation assay for the detection of eubacteria - esp  
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
XX  
XX Claim 5; Fig 57; 248pp; English.

CC The sequences given in AAT11889-905 represent the 16S-23S rRNA spacer  
CC regions derived from various microorganisms. These sequences were  
CC used in the method of the invention for the detection and identification  
CC of at least one or more microorganisms. The method comprises amplifying  
CC the 16S-23S rRNA spacer region and hybridising one or more probes to  
CC the amplified sequence. These probes were specifically used to detect  
CC microorganisms in samples originating from food. This spacer region is  
CC derived from Brucella suis NIDO Biovar 1.

XX Sequence 808 BP; 177 A; 181 C; 237 G; 210 T; 3 other;

Query Match 22.3%; Score 104.4; DB 17; Length 808;  
Best Local Similarity 79.0%; Pred. No. 4.9e-23;  
Matches 139; Conservative 0; Mismatches 31; Indels 6; Gaps 1;

QY 84 TGGGCTGTAGCTCAGTTGGTTAGAGCGCACACCGCTTATAGCGTGGGGTCGGAGGTTCAA 143

DB 279 TGGGCTGTAGCTCAGTTGGTTAGAGCGCACACCGCTTATAGCGTGGGGTCGGAGGTTCAA 338

QY 144 ATCTGCCAGACCCACCAATTGCT-----GGGGCCATAGCTCAGCTGGGAGAGCGCCT 197

DB 339 GTCTCCAGAGCGCCACCAAGTTACTTGTATGAGGGCGGTAGCTCAGCTGGGAGAGCACCT 398

QY 198 GCCTTCACGAGGAGGTGACGGTTGATCCCGCTTGGCTCCACACCCCGCTTG 253

DB 399 GCTTTCAGAGAGGGGGTCTGGTTGATCCCGCTTGGCTCCACCATCATGTTGG 454

RESULT 15

AAT11891

ID AAT11891 standard; DNA; 809 BP.

XX AC AAT11891;

XX

DT 03-SEP-1996 (first entry)

XX

DE Brucella abortus NIDO Tulya Biovar 3 16S-23S rRNA spacer region.

XX

KW Probe; detection; identification; microorganism; amplify;

XX 16S-23S rRNA spacer region; food; universal;

XX species-specific; ss.

OS Brucella abortus.

XX

PN WO9600298-A1.

XX

PD 04-JAN-1996.

XX

PF 23-JUN-1995; 95WO-EP02452.

XX

PR 07-APR-1995; 95EP-0870032.

XX 24-JUN-1994; 94EP-0870106.

XX (INNO-) INNOGENETICS NV.

XX

PI Jannes G, Rossau R, Van Heuverswyn H;

XX

DR WPI; 1996-068882/07.

XX

XX Novel hybridisation assay for the detection of eubacteria - esp  
PT Mycobacterium, comprises amplifying the 16S-23S rRNA spacer region  
XX  
XX Claim 5; Fig 79; 248pp; English.

XX

CC The sequences given in AAT11889-905 represent the 16S-23S rRNA spacer  
CC regions derived from various microorganisms. These sequences were  
CC used in the method of the invention for the detection and identification  
CC of at least one or more microorganisms. The method comprises amplifying  
CC the 16S-23S rRNA spacer region and hybridising one or more probes to  
CC the amplified sequence. These probes were specifically used to detect  
CC microorganisms in samples originating from food. This spacer region is  
CC derived from Brucella abortus NIDO Tulya biovar 3.

XX Sequence 809 BP; 179 A; 181 C; 236 G; 211 T; 2 other;

Query Match 22.3%; Score 104.4; DB 17; Length 809;  
Best Local Similarity 79.0%; Pred. No. 4.9e-23;  
Matches 139; Conservative 0; Mismatches 31; Indels 6; Gaps 1;

QY 84 TGGGCTGTAGCTCAGTTGGTTAGAGCGCACACCGCTTATAGCGTGGGGTCGGAGGTTCAA 143

DB 280 TGGGCTGTAGCTCAGTTGGTTAGAGCGCACACCGCTTATAGCGTGGGGTCGGAGGTTCAA 339

QY 144 ATCTGCCAGACCCACCAATTGCT-----GGGGCCATAGCTCAGCTGGGAGAGCGCCT 197

DB 340 GTCTCCAGAGCGCCACCAAGTTACTTGTATGAGGGCGGTAGCTCAGCTGGGAGAGCACCT 399

QY 198 GCCTTCACGAGGAGGTGACGGTTGATCCCGCTTGGCTCCACACCCCGCTTG 253

DB 400 GCTTTCAGAGAGGGGGTCTGGTTGATCCCGCTTGGCTCCACCATCATGTTGG 455

Search completed: February 1, 2003, 01:41:23

Job time : 343.822 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:17:06 ; Search time 24.3314 Seconds  
(without alignments)  
5898.736 Million cell updates/sec

Title: US-09-931-486-115  
Perfect score: 468  
Sequence: 1 ATCGACGACATCAGCTGTCT.....CAGATTGCTGGGGTTATAT 468

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2.6/ptodata/1/ina/5B-COMB.seq.\*  
3: /cgn2.6/ptodata/1/ina/6A-COMB.seq.\*  
4: /cgn2.6/ptodata/1/ina/6B-COMB.seq.\*  
5: /cgn2.6/ptodata/1/ina/PCTUS-COMB.seq.\*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	468	100.0	468	3	US-08-765-332-115	Sequence 115, App
2	468	100.0	468	4	US-09-448-894-115	Sequence 115, App
3	216	46.2	471	3	US-08-765-332-111	Sequence 111, App
4	216	46.2	471	4	US-09-448-894-111	Sequence 111, App
5	205.2	43.8	504	3	US-08-765-332-113	Sequence 113, App
6	205.2	43.8	504	4	US-09-448-894-113	Sequence 113, App
7	198.4	42.4	499	3	US-08-765-332-114	Sequence 114, App
8	198.4	42.4	499	4	US-09-448-894-114	Sequence 114, App
9	178	38.0	520	3	US-08-765-332-112	Sequence 112, App
10	178	38.0	520	4	US-09-448-894-112	Sequence 112, App
11	109	23.3	603	1	US-08-412-614-85	Sequence 85, App
12	109	23.3	603	1	US-08-412-614-86	Sequence 86, App
13	109	23.3	603	2	US-08-635-761-85	Sequence 85, App
14	109	23.3	603	2	US-08-635-761-86	Sequence 86, App
15	109	23.3	603	4	US-09-312-520-85	Sequence 85, App
16	109	23.3	603	4	US-09-312-520-86	Sequence 86, App
17	104.8	22.4	664	1	US-08-412-614-89	Sequence 89, App
18	104.4	22.3	808	3	US-08-765-332-131	Sequence 131, App
19	104.4	22.3	808	3	US-08-765-332-132	Sequence 132, App
20	104.4	22.3	808	4	US-09-448-894-131	Sequence 131, App
21	104.4	22.3	808	4	US-09-448-894-132	Sequence 132, App
22	104.4	22.3	809	3	US-08-765-332-154	Sequence 154, App
23	104.4	22.3	809	4	US-09-448-894-154	Sequence 154, App
24	100.8	21.5	549	1	US-08-412-614-92	Sequence 92, App
25	100.8	21.5	549	2	US-08-635-761-92	Sequence 92, App
26	100.8	21.5	549	4	US-09-312-520-92	Sequence 92, App
27	99.4	21.2	498	1	US-08-412-614-90	Sequence 90, App

28 99.4 21.2 498 2 US-08-635-761-90 Sequence 90, Appl  
29 99.4 21.2 498 4 US-09-312-520-90 Sequence 90, Appl  
30 96 20.5 470 3 US-08-765-332-195 Sequence 195, App  
31 96 20.5 470 4 US-09-448-894-195 Sequence 195, App  
32 89 19.0 582 1 US-08-412-614-87 Sequence 87, Appl  
33 89 19.0 582 2 US-08-635-761-87 Sequence 87, Appl  
34 89 19.0 582 4 US-09-312-520-87 Sequence 88, Appl  
35 89 19.0 590 1 US-08-412-614-88 Sequence 88, Appl  
36 89 19.0 590 2 US-08-635-761-88 Sequence 88, Appl  
37 89 19.0 590 4 US-09-312-520-88 Sequence 88, Appl  
38 88.4 18.9 463 3 US-08-765-332-215 Sequence 215, App  
39 88.4 18.9 463 4 US-09-448-894-215 Sequence 215, App  
40 88.4 18.9 475 3 US-08-765-332-214 Sequence 214, App  
41 88.4 18.9 475 4 US-09-448-894-214 Sequence 214, App  
42 87 18.6 654 2 US-08-635-761-89 Sequence 89, Appl  
43 87 18.6 654 4 US-09-312-520-89 Sequence 89, Appl  
44 78.6 16.8 363 3 US-08-765-332-119 Sequence 119, App  
45 78.6 16.8 363 4 US-09-448-894-119 Sequence 119, App

## ALIGNMENTS

RESULT 1  
US-08-765-332-115  
; Sequence 115, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 468 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

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; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-765-332-115

Query Match      100.0%; Score 468; DB 3; Length 468;
Best Local Similarity 100.0%; Pred. No. 9.4e-152;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCGACGACATCAGCTGCTCATAGCTCCACAGCAATTCGCTGATTCATTGAAGAAGA 60
Db 1 ATCGACGACATCAGCTGCTCATAGCTCCACAGCAATTCGCTGATTCATTGAAGAAGA 60
Qy 61 CGATTAGGTAGCAACCTTCGATGGGCTCTAGCTAGCTAGTGGTGTAGAGCGCACCCCTGA 120
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Qy 121 TAAGGGTGAGGTCGGCAGTTTCTGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCT 180
Db 121 TAAGGGTGAGGTCGGCAGTTTCTGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCT 180
Qy 181 CAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTCAGCGGTTGATCCCGCTTGGCTCC 240
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Qy 241 ACCACCCGCTTGCAGTTTCTGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCT 300
Db 241 ACCACCCGCTTGCAGTTTCTGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCT 300
Qy 301 TCTGAACCTTATCAGATCGTTCCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 420
Db 301 TCTGAACCTTATCAGATCGTTCCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 420
Qy 421 TCGGCGAATGTTGCTTCCACAGTATAACAGATTGCTTGGGGTTATAT 468
Db 421 TCGGCGAATGTTGCTTCCACAGTATAACAGATTGCTTGGGGTTATAT 468

RESULT 2
US-09-448-894-115
; Sequence 115, Application US/09448894
; Patent No. 6312903
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY

NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22201

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,894
; FILING DATE: 29-NOV-1999
; CLASSIFICATION: <Unknown>
; 07-APR-1995
; 24-JUN-1994
; PRIOR APPLICATION DATA:
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY
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; APPLICATION NUMBER: 08/765,332
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95870032.0
; FILING DATE: 07-APR-1995
; APPLICATION NUMBER: EP 94870106.5
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-448-894-115

Query Match      100.0%; Score 468; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 9.4e-152;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCGACGACATCAGCTGCTCATAGCTCCACAGCAATTCGCTGATTCATTGAAGAAGA 60
Db 1 ATCGACGACATCAGCTGCTCATAGCTCCACAGCAATTCGCTGATTCATTGAAGAAGA 60
Qy 61 CGATTAGGTAGCAACCTTCGATGGGCTCTAGCTAGCTAGTGGTGTAGAGCGCACCCCTGA 120
Db 61 CGATTAGGTAGCAACCTTCGATGGGCTCTAGCTAGCTAGTGGTGTAGAGCGCACCCCTGA 120
Qy 121 TAAGGGTGAGGTCGGCAGTTTCTGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCT 180
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Qy 241 ACCACCCGCTTGCAGTTTCTGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCT 300
Db 241 ACCACCCGCTTGCAGTTTCTGAATCTGCCAGACCCACCAATTTGCTGGGGCCATAGCT 300
Qy 301 TCTGAACCTTATCAGATCGTTCCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 420
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Qy 421 TCGGCGAATGTTGCTTCCACAGTATAACAGATTGCTTGGGGTTATAT 468
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RESULT 3
US-08-765-332-111
; Sequence 111, Application US/08765332
; Patent No. 6025132
; GENERAL INFORMATION:
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; APPLICANT: VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
; HYBRIDIZATION ASSAY
```

NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 471 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-111

Query Match 46.2%; Score 216; DB 3; Length 471;  
Best Local Similarity 74.9%; Pred. No. 8.4e-65;  
Matches 370; Conservative 0; Mismatches 75; Indels 49; Gaps 6;  
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Db 1 ATCGAAGATCCGGCTTCTTCTATAGCTCCACACGAAATTCCTTGAATTCATTGAAGAAGA 59  
QY 61 CGATTAGTTAGCAACCTTCGATTGGTGTGTAGCTCAGTTGGTTAGAGCCACCCCTGA 120  
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QY 121 TAAGGGTGAGTCCGGAGTTCGAAATCGCCAGACCCACCAATTT----- 164  
Db 101 TAAGGGTGAGTCCGGAGTTCGAAATCGCCAGACCCACCAATTTGGTGTGTGGGTG 160  
QY 165 -----TGCCTGGGGCCATAGCTAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTGAGC 219  
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Db 338 GTATGTGATAGAAAGTAACTGAATGATCTCTTTCCACGGTGTGATTCATTCAGTCAAGTA 397  
QY 397 AAATTTGTGAGT--AAATACAAAGTTTTGGCGAATGTTGTTCTTCACAGTATACAGAGATT 454  
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QY 455 GCTTGGGGTTATAT 468  
Db 458 GCTTGGGGTTATAT 471  
RESULT 4  
US-09-448-894-111  
Sequence 111, Application US/09448894  
Patent No. 6312903  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
ROSSAU, RUDI  
VAN HEUVERSWEYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-6312903-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 471 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 111:  
US-09-448-894-111

Query Match 46.2%; Score 216; DB 4; Length 471;  
Best Local Similarity 74.9%; Pred. No. 8.4e-65;  
Matches 370; Conservative 0; Mismatches 75; Indels 49; Gaps 6;

QY 1 ATCGACGACATCAGCTGTCTCATAGTCCACACGAAATTCCTTGAATTCATTGAAGAAGA 60

Db 1 ATCGAAGATCCGGCTCTTCTATAGCTCCACAGCAATGCTGATTCACCTGGTTAGA- 59  
Qy 61 CGATTAGGTAGCAACCTTCGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTCA 120  
Db 60 -----CGATTGGGCTGTGTAGCTCAGTTGGTTAGAGCGCACCCCTGA 100  
Qy 121 TAAGGTGAGGTGGCAGTTCGAATCTGCCAGACCCACCAAT----- 164  
Db 101 TAAGGTGAGGTGGCAGTTCGAATCTGCCAGACCCACCAATTTGTTGGTGTGCGTG 160  
Qy 165 -----TGTGGGGCCATAGCTCAGCTGGGAGAGCGCTTGTGACGAGAGGTGACG 219  
Db 161 ATCCGATACGGGGCCATAGCTCAGCTGGGAGAGCGCTTGTGACGAGAGGTGACG 220  
Qy 220 GGTTCGATCCCGCTGGCTCCACCGCCCGCTTGCACAGTTTCAAGCTTAGAATGAA 279  
Db 221 AGTTCGATCCCTCTGGCTCCACCAT-----TAAACAAATCTCGAAGCTCAGAAATGAA 277  
Qy 280 TATTCG-CGTCAATATTGATTCTGAATTT-ATCAGAATCGTTCTTTAAAAATTTGG 336  
Db 278 TGTTCGTGATGAACATGATTCTGTGCTTGTGACCAAGACTGTTCTTTAAAAATTCGG 337  
Qy 337 GTATGTATAGAAAGATAGACTGGACAGCACTTTCACCTGGTGTGTTTACAGCTAAGTA 396  
Db 338 GTATGTATAGAAAGATAGACTGAATGATCTCTTTCACCTGGTGTGATCATTCAGTCAAGTA 397  
Qy 397 AATTTGTGAGT--AATTACAAGTTTTCGGCGAATGTTGCTTCACAGTATTAACAGATT 454  
Db 398 AATTTGGGAGTTCAAGCGCGAATTTTGGCGAATGTGCTTCACAGTATAACAGATT 457  
Qy 455 GCTTGGGGTTATAT 468  
Db 458 GCTTGGGGTTATAT 471

## RESULT 5

US-08-765-332-113  
; Sequence 113, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P. C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765.332  
; FILING DATE: 23-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/02452  
; FILING DATE: 23-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994

## ; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 113:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 504 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-765-332-113

Query Match 43.8%; Score 205.2; DB 3; Length 504;

Best Local Similarity 74.7%; Pred. No. 4.7e-61;

Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;

Qy 1 ATCGAGCATCAGCTGTCTCATAGCTCCACACGAATTCGTTGATTCATCA-TTGAAGAAG 59  
Db 1 ATCGAAGACACCGGCTTCGTCTATAAGCTCCACAGCAATTCGTTGATTCACCTTCGGAAG 60  
Qy 60 ACGATTAGTTAGCAACCTT-----CGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCA 113  
Db 61 GCGATTGGTTAGACCCGAGAGTAACGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 120  
Qy 114 CCCCTGATAAGGTTGAGGTGGCAGTTTCGAATCTGCCAGACCCACCAATTTGCTGGGGC 173  
Db 121 CCCCTGATAAGGTTGAGGTGGCAGTTTCGAATCTGCCAGACCCACCA-TCGAAGGGGC 179  
Qy 174 CATAGCTCAGTGGAGAGCGGCTGCTTGCAGCAGGAGGTGAGGGGTCGATCCCGCT 233  
Db 180 CATAGCTCAGTGGAGAGCGGCTGCTTGCAGCAGGAGGTGAGGGGTCGATCCCGCT 239  
Qy 234 TGGCTCCAC-----ACCCCGCTTCCAGTTTGTCAAAGCTTAGAA 274  
Db 240 TGGCTCCACCAATTAAGTCTAGTCGCGCAAGCTCAGAAATGAGTTTACCAGGATGAGG 299  
Qy 275 ATGAATATTCGCTCGAATATTGATTTCTGAATTT--ATCAGAATCGTTCTTTAAAAAT 332  
Db 300 TTGATTGCTGGTTCGAACATTTGATTTCTGACTTTTCCGCCAGCACTGTTCTTTAAAAAT 359  
Qy 333 TTGGGTATGTATAGAAAGATAGACGACACTTTTCACTGGTGTGTTTCAGGCTAA 392  
Db 360 TTGGGTATGTATAGAAAGTAGA-CCGATGTGTGCTTTTCACTGGCAGCATGTCGCGTCAA 418  
Qy 393 GGTAAATTTGTGAGTAAT---TACAAGTTTTCGGGCAATGTTGCTTTCACAGTA----- 444  
Db 419 GGTAAATTTGTGAGTCTCTATGCAAAATTTTCGGGCAATGTCGCTTTCACGTTATAGAC 478  
Qy 445 --TAACCAAGATTGCTTGGGGTTATAT 468  
Db 479 AGTAACCAAGATTGCTTGGGGTTATAT 504

## RESULT 6

US-09-448-894-113  
; Sequence 113, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P. C.



STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Query Match 43.8%; Score 205.2; DB 4; Length 504;  
Best Local Similarity 74.7%; Pred. No. 4.7e-61;  
Matches 378; Conservative 0; Mismatches 88; Indels 40; Gaps 8;

QY 1 ATCGAGCATCAGCTGCTCATAAGTCCACAGCAATGCTTGATCA-TTGAAGAG 59  
DB 1 ATCGAGACACCGGCTTCGTATAAGTCCACAGCAATGCTTGATCACTTGGCAAG 60

QY 60 ACGATTAGGTTAGCAACCTT-----CGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA 113  
DB 61 GCGATTGGTTAGACCCGAGAGTAACGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA 120

QY 114 CCCCTGATAAGGTGAGTGGCAGTTCGAATCTCCAGACCCACCAATTTGCTGGGCG 173  
DB 121 CCCCTGATAAGGTGAGTGGCAGTTCGAATCTCCAGACCCACCAATTTGCTGGGCG 179

QY 174 CATAGCTCAGCTGGGAGAGCGCTCCCTTGGACGAGGAGTCCAGTCCCGCT 233  
DB 180 CATAGCTCAGCTGGGAGAGCGCTCCCTTGGACGAGGAGTCCAGTCCCGCT 239

QY 234 TGGCTCCACC-----ACCCCGCTTGGCAAGTTGTCAAAGCTTAGAA 274  
DB 240 TGGCTCCACCATAACTAGTCGCGGAAAGCTCAGAATGAGTGTACAGGATGAGG 299

QY 275 ATGAATATTCGGTGCATATGATTCTGAATTT--ATCAATATCGTTCTTTAAAT 332  
DB 300 TTGATTGCTGGTGAACATGATTCTTGGACTTTGGCCAGAACTGTTCTTTAAAT 359

QY 333 TTGGTATGATAGAAAGATAGACTGGACAGCACTTTCACTGGTGTGTTCAGCGTAA 392  
DB 360 TTGGTATGATAGAAAGTAGA-CCGATGTGTGTCTTCACTGGGAGCATGTGCGGTCAA 418

QY 393 GGTAAATTTGTGAGTAAT---TACAAGTTTTCGGCAATGTGTTCTTCACAGTA----- 444  
DB 419 GGTAAATTTGCGTGTCTCTATGCAAAATTTTCGGCAATGTGTTCTTCACGTATAGAC 478

QY 445 --TAACCAGATTGCTTGGGGTTATAT 468  
DB 479 AGTAACCAGATTGCTTGGGGTTATAT 504

RESULT 7  
US-08-765-332-114  
; Sequence 114, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; TITLE OF INVENTION: HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
NAME: SADOFF, B.J.  
ATTORNEY/AGENT INFORMATION:  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-114

Query Match 42.4%; Score 198.4; DB 3; Length 499;  
Best Local Similarity 72.8%; Pred. No. 1e-58;  
Matches 367; Conservative 0; Mismatches 96; Indels 41; Gaps 7;

QY 1 ATCGAGCATCAGCTGCTCATAAGTCCACAGCAATGCTTGATTCATTCAGAAAGA 60  
DB 1 ATCGAGACTTCAGCTTCTTATAGTCCACAGCAATGCTTGATTCATTCAGAAAGA 60

QY 61 CGATTAGGTTAGCAACCTT-----CGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 113  
| | | | |  
Db 61 GCAGTTGGGTTGAGACCCGAGAGTGACGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA 120  
| | | | |  
QY 114 CCCTGATAGAGGTGAGGTGGGAGTTCGATCTGCCAGACCCAGACCAATTTGC----- 167  
| | | | |  
Db 121 CCCTGATAGAGGTGAGGTGGGAGTTCGATCTGCCAGACCCAGACCAATTTGC----- 180  
| | | | |  
QY 168 -----TGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTCACGCGAGGAGGT 215  
| | | | |  
Db 181 GCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTCACGCGAGGAGGT 240  
| | | | |  
QY 216 CAGCGGTTGATCCCGCTTGGCTCCACACCCCGCTTGGCAGTTTGTCAAAAGCTTAGAAA 275  
| | | | |  
Db 241 CAGGAGTTGATCCCTTGGCTCCACCA--TCAACTCAGCATCGCTGAAAGCTCAGAAA 298  
| | | | |  
QY 276 TGAATATTCG-CGTGCAATATGATTTCTGAACCTT--ATCAGAAATCGTTCTTAAATAAT 332  
| | | | |  
Db 299 TGAACATTTGATGTTCAATGTTGATTTCTGCTTTCGCGAGAACTGTTCTTTAAATAAT 358  
| | | | |  
QY 333 TTGGGTATGTGATAGAAAGATAGACTGCAGACGACTTTTCACTGCTGTGTTTCAAGGCTAA 392  
| | | | |  
Db 359 TTGGGTATGTGATAGAAAGATAGACTGCAGACGACTTTTCACTGCTGTGTTTCAAGGCTAA 415  
| | | | |  
QY 393 GGTAAATTTGATGATTAATACAGTTTTCGGCGAAATGTTGTCTTTCAC-----AGTA 444  
| | | | |  
Db 416 CAAAATTTGCGAGTTCAAGCGCGAAATTTTCGGCGAAATGTTGTCTTTCACGAATCTA 475  
| | | | |  
QY 445 TAACACAGATTGCTTGGGGTTATAT 468  
| | | | |  
Db 476 TAACACAGATTGCTTGGGGTTATAT 499  
| | | | |

## RESULT 8

US-09-448-894-114  
; Sequence 114, Application US/09448894  
; Patent No. 6312903  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; VAN HEUVERSWYN, HUGO  
; ROSSAU, RUDI  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/448,894  
; FILING DATE: 29-Nov-6312903-1999  
; CLASSIFICATION: <Unknown>  
; 07-APR-1995  
; 24-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/765,332  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: EP 95870032.0  
; FILING DATE: 07-APR-1995  
; APPLICATION NUMBER: EP 94870106.5  
; FILING DATE: 24-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663

; REFERENCE/DOCKET NUMBER: 1487-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 114:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 499 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:  
; US-09-448-894-114

Query Match 42.4%; Score 198.4; DB 4; Length 499;  
Best Local Similarity 72.8%; Pred. No. 1e-58;  
Matches 367; Conservative 0; Mismatches 96; Indels 41; Gaps 7;

QY 1 ATCGACGACATCAGCTGTCTCATAAGCTCCACACGAATTCGTTGATTCATTTGAAGAAGA 60  
| | | | |  
Db 1 ATCGAAGACTTCAGCTTCTTCATAAGTTCACACAGAAATTCGTTGATTCATTCGGAAGA 60  
| | | | |  
QY 61 CGATTAGGTTAGCAACCTT-----CGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCA 113  
| | | | |  
Db 61 GCGATTGGGTTGAGACCCGAGAGTGACGATTGGGCTGTAGCTCAGTTGGTTAGAGCGCA 120  
| | | | |  
QY 114 CCCCTGATAGGTTGAGTTCGGCAGTTTCGAATCTGCCACACCCACCAATTTGC----- 167  
| | | | |  
Db 121 CCCCTGATAGGTTGAGTTCGGCAGTTTCGAATCTGCCACACCCACCAATTTGTGCGGATG 180  
| | | | |  
QY 168 -----TGGGCGCATAGCTCAGCTGGGAGAGCGCTGCTTCACGCGAGGAGGT 215  
| | | | |  
Db 181 GCCAGTGTCAAAATGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTCACGCGAGGAGGT 240  
| | | | |  
QY 216 CAGCGGTTGATCCCGCTTGGCTCCACACCCCGCTTGGCAGTTTGTCAAAAGCTTAGAAA 275  
| | | | |  
Db 241 CAGGAGTTGATCCCTTGGCTCCACCA--TCAACTCAGCATCGCTGAAAGCTCAGAAA 298  
| | | | |  
QY 276 TGAATATTCG-CGTGCAATATGATTTCTGAACCTT--ATCAGAAATCGTTCTTAAATAAT 332  
| | | | |  
Db 299 TGAACATTTGATGTTCAATGTTGATTTCTGCTTTCGCGCAGAACTGTTCTTTAAATAAT 358  
| | | | |  
QY 333 TTGGGTATGTGATAGAAAGATAGACTGCAGACGACTTTTCACTGCTGTGTTTCAAGGCTAA 392  
| | | | |  
Db 359 TTGGGTATGTGATAGAAAGATAGACTGCAGACGACTTTTCACTGCTGTGTTTCAAGGCTAA 415  
| | | | |  
QY 393 GGTAAATTTGATGATTAATACAGTTTTCGGCGAAATGTTGTCTTTCAC-----AGTA 444  
| | | | |  
Db 416 CAAAATTTGCGAGTTCAAGCGCGAAATTTTCGGCGAAATGTTGTCTTTCACGAATCTA 475  
| | | | |  
QY 445 TAACACAGATTGCTTGGGGTTATAT 468  
| | | | |  
Db 476 TAACACAGATTGCTTGGGGTTATAT 499  
| | | | |

## RESULT 9

US-08-765-332-112  
; Sequence 112, Application US/08765332  
; Patent No. 6025132  
; GENERAL INFORMATION:  
; APPLICANT: JANNES, GEERT  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
; AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
; HYBRIDIZATION ASSAY  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: WASHINGTON

STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,332  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/02452  
FILING DATE: 23-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4100  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-765-332-112

Query Match 38.0%; Score 178; DB 3; Length 520;  
Best Local Similarity 71.1%; Pred. No. 1.2e-51;  
Matches 371; Conservative 0; Mismatches 95; Indels 56; Gaps 8;

Qy 1 ATCGACGACATCAGCTGTCTCATAGCTCCACAGCAATGCTTGCATTCATTGAAGAAGA 60  
Db 1 ATCGAAGACATCAGCTTCTCATAGTATCCACAGCAATGCTTGCATTCATTGAAGAAGA 60

Qy 61 CGATTAGTTAGCAACCTTCGAT-TGGGTCGTAGCTCAGTTGGTTAGAGCGCACCCCTG 119  
Db 61 AATGCTGTAAACGCGACCGCTGTATAGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTG 120

Qy 120 ATAAGGTTAGGTCGGCAGTTGCAATCTGCCAGCACCCACCAATTTGCT----- 168  
Db 120 ATAAGGTTAGGTCGGCAGTTGCAATCTGCCAGCACCCACCAATTTGCT----- 168

Qy 169 -----GGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTCAGCGGTC 224  
Db 181 ATACGGGGCCATAGCTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGTCAGCGGTC 240

Qy 225 GATCCGCTTGGCTCCACCAACC-----CGCTTGCACAGTTTGCAAGCTTAGAAATG 277  
Db 241 GATCCGCTTGGCTCCACCAACCCTCTCGTTGGGTCAGTTGTTAAAGAGTCAGAAATG 300

Qy 278 A-----ATATTCGGTTCGAATTTGATTCGAACTT-----TATCAGAA 317  
Db 301 ATGCGGCTCAGGTTGTCCTGTTGAGTGCTGATTTCTGGCTTTGACCGGTACGAAAA 360

Qy 318 TCGTCTTTAAAAATTTGGGTATGTGATAGAAAGATAGACTGGACAGCACTTTTCACTGGT 377  
Db 361 TCGTCTTTAAAAATTTGGGTATGTGATAGAAAGATAGACTGGATTAATG--CTTCACTGGC 418

Qy 378 GTGTGTCAGGCTAAGGTAAATTTGTGAGT-----AATTAAGTTTTTCGGCGAATGTTG 433  
Db 378 GTGTGTCAGGCTAAGGTAAATTTGTGAGT-----AATTAAGTTTTTCGGCGAATGTTG 433

Db 419 AATTGATCTGTCAGGTAATAATTTGTAGTTCTTCAAGACGCAAAATTTTCGGCGAATGTCG 478

Qy 434 TCTTCAC-----AGTATAACCAAGATTCCTTTGGGGTTATAT 468  
Db 479 TCTTCACGATTCAGACAGTAACCAAGATTCCTTTGGGGTTATAT 520

RESULT 10  
US-09-448-894-112  
Sequence 112, Application US/09448894  
Patent No. 6312903  
GENERAL INFORMATION:  
APPLICANT: JANNES, GEERT  
ROSSAU, RUDI  
VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A  
HYBRIDIZATION ASSAY  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,894  
FILING DATE: 29-NOV-6312903-1999  
CLASSIFICATION: <Unknown>  
07-APR-1995  
24-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,332  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 95870032.0  
FILING DATE: 07-APR-1995  
APPLICATION NUMBER: EP 94870106.5  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 112:  
US-09-448-894-112

Query Match 38.0%; Score 178; DB 4; Length 520;  
Best Local Similarity 71.1%; Pred. No. 1.2e-51;  
Matches 371; Conservative 0; Mismatches 95; Indels 56; Gaps 8;

Qy 1 ATCGACGACATCAGCTGTCTCATAGCTCCACAGCAATGCTTGCATTCATTGAAGAAGA 60  
Db 1 ATCGAAGACATCAGCTTCTCATAGTATCCACAGCAATGCTTGCATTCATTGAAGAAGA 60

Qy 61 CGATTAGTTAGCAACCTTCGAT-TGGGTCGTAGCTCAGTTGGTTAGAGCGCACCCCTG 119  
Db 61 AATGCTGTAAACGCGACCGCTGTATAGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTG 120

Db 61 AATGCTGTAACGCGACCCCGTGTATAGGCTGTAGCTAGTGGTTAGAGCGACCCCTG 120  
QY 120 ATAAGGCTGAGGTGCGCAGTTCGAATCTGCCAGACCCACCAATTTGCT----- 168  
Db 121 ATAAGGCTGAGGTGCGCAGTTCGAATCTGCCAGACCCACCAATTTGCTGGTTCGAGAAGA 180  
QY 169 ----GGGGCCATAGCTACGTACGTGGGAGAGCGCCCTTGCACGACGAGGTTCACGCGTTC 224  
Db 181 ATACGGGGCCATAGCTACGTACGTGGGAGAGCGCCCTTGCACGACGAGGTTCACGCGTTC 240  
QY 225 GATCCCGCTTGGCTCCACACCC-----CGCTTCCAGTGTGTCAAGACCTAGAAATG 277  
Db 241 GATCCCGCTTGGCTCCACACCTCTCTCGTGTGCGGTGAGTGTAAAGAGTTCAGAAATG 300  
QY 278 A-----ATATTCGCGTCGAATATGATTTCTGAACCT-----TATCAGAA 317  
Db 301 ATGCCGCTTCAGGTTGCTGTTGAGTGTGATTTCTGCTTTGACCGGTACGAAAA 360  
QY 318 TCCTTCTTTAAATTTGGGTATGTGATAGAAAGATAGACTGACAGCACTTTCACTGGT 377  
Db 361 TCCTTCTTTAAATTTGGATATGTGATAGAGTGTGATTAATG--CTTTCACTGGC 418  
QY 378 GTGTGTTTACGGCTAAGTAAATTTCTGAGT---AATTACAGTTCGCGGAATGTTG 433  
Db 419 AATTGATCTGGTCAAGTAAATTTCTGAGT---AATTACAGTTCGCGGAATGTTG 478  
QY 434 TCTTCAC-----AGTATAACACAGATGCTTTGGGGTTATAT 468  
Db 479 TCTTCAGATTGACAGAGTAAACAGATGCTTTGGGGTTATAT 520

RESULT 11  
US-08-412-614-85  
; Sequence 85, Application US/08412614  
; Patent No. 5536638  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: Hybridization Probes Derived from the  
; TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the  
; TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5536638west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402-4131  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity  
; COMPUTER: IBM PC compatible (Compaq Deskpro 286e)  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect Version #5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/412,614  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,394  
; FILING DATE: 17-DEC-1992  
; APPLICATION NUMBER: PCT/EP91/00743  
; FILING DATE: 18-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB/90901054.3  
; FILING DATE: 18-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A.  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076,75-USWO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081

; INFORMATION FOR SEQ ID NO: 85:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 603 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Neisserai gonorrhoeae  
; STRAIN: NCTC 8375  
; US-08-412-614-85  
  
Query Match 23.3%; Score 109; DB 1; Length 603;  
Best Local Similarity 62.5%; Pred. No. 8.1e-28;  
Matches 187; Conservative 0; Mismatches 110; Indels 2; Gaps 1;  
  
QY 85 GGTCTGTAGCTCAGTTGTTAGAGCGACCCCTGTATAGGGTGGAGTTCGGCAGTTCCGAA 144  
Db 99 GGTCTGTAGCTCAGTTGTTAGAGCGACCGCTTGTATAGCGTGGAGTTCGGAGGTTCAAG 158  
QY 145 TCTGCCAGACCCACCAATTTGCTGGGGCCATAGCTCAGCTGGAGAGCGCTGCCCTTGC 204  
Db 159 TCTCCAGACCCACCA--GAACGGGGGCTAGCTAGTGGTAGAGCACTGCTTGC 216  
QY 205 ACCGAGAGTCAAGCGTTTCGATCCCGCTTGGCTCCACACCGCTTGCAGTTGTCA 264  
Db 217 AAGCAGGGGCTCATCGTTTCGATCCCGTTTGCCTCCACCAAACTTTACAAATGAAAGCA 276  
QY 265 AAGCTTAGAATGAATATTCGCGTCGAAATATTGATTTCTGCACTTTATCAGATCGTCT 324  
Db 277 AGTTTCTGTTTTCAGCAGCTTATTTTTCGGAAGTAGAATAAGCAGCATCGAICT 336  
QY 325 TTAATAATTTGGTATGTGATAGAAAGATAGACTGGACAGCACTTTCACTGGTGTGTGT 383  
Db 337 TTAACAAATTGGAAAGCCGGAATCAACAAACAAAGACATGAGTTGTTGATTTTTT 395  
  
RESULT 12  
US-08-412-614-86  
; Sequence 86, Application US/08412614  
; Patent No. 5536638  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: Hybridization Probes Derived from the  
; TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the  
; TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5536638west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402-4131  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity  
; COMPUTER: IBM PC compatible (Compaq Deskpro 286e)  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect Version #5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/412,614  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,394  
; FILING DATE: 17-DEC-1992  
; APPLICATION NUMBER: PCT/EP91/00743  
; FILING DATE: 18-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB/90901054.3

FILING DATE: 18-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75-USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Neisseria gonorrhoeae  
STRAIN: ITM 4367  
US-08-412-614-86

Query Match 23.3%; Score 109; DB 1; Length 603;  
Best Local Similarity 62.5%; Pred. No. 8.1e-28;  
Matches 187; Conservative 0; Mismatches 110; Indels 2; Gaps 1;  
QY 85 GGCTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGTTGAGTGGCGAGTTTCGAA 144  
|||||  
Db 99 GGGTTTGTAGCTCAGTTGGTTAGAGCACACGCTTGATAAGCGTTGAGTGGCGAGTTTCGAA 158  
QY 145 TCTGCCAGACCCACCAATTTGCTGGGCGCATAGCTCAGCTGGGAGAGCGCCCTGCTTGC 204  
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Db 159 TCTCCAGACCCACCAA--GAACGGGGCATAGCTCAGTTGGTAGAGCACCTGCTTGC 216  
QY 205 AGCAGAGGTGAGGTTGATCCGCTGGCTCCACACCCCGCTTGCAGTTTGTCA 264  
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Db 217 AAGCAGGGGTGATCGATCCGCTTGGCTCCACCAAACTTTACAAATGAAAGCA 276  
QY 265 AAGCTTAGAAATGAATATTCGCGTGAATATTGATTTCGAACTTTATCAGATCGTTCT 324  
Db 277 AGTTTCTGTTTACGAGCTTATTTGATTTCGAGTAGAATAGCAGCATCATCT 336  
QY 325 TTAATAATTTGGTATGATAGAAAGATAGACTGGACAGCACTTTCACTGGTGTGT 383  
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Db 337 TTAACAAATTTGAAAGCCGAAATCAACAAAGACAAATGAGTTGTTTGTATTTT 395

RESULT 13  
US-08-635-761-85

Sequence 85, Application US/08635761  
Patent No. 5945282  
GENERAL INFORMATION:  
APPLICANT: Rossau, Rudi  
TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
STREET: 3100 No. 5945282 West Center, 90 S. 7th Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: U.S.A.  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/635,761  
FILING DATE: 19-APR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,394

FILING DATE: 17-DEC-1992  
APPLICATION NUMBER: 08/412,614  
FILING DATE: 29-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75USC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/332-5300  
TELEFAX: 612/332/9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-635-761-85

Query Match 23.3%; Score 109; DB 2; Length 603;  
Best Local Similarity 62.5%; Pred. No. 8.1e-28;  
Matches 187; Conservative 0; Mismatches 110; Indels 2; Gaps 1;  
QY 85 GGCTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGTTGAGTGGCGAGTTTCGAA 144  
|||||  
Db 99 GGGTTTGTAGCTCAGTTGGTTAGAGCACACGCTTGATAAGCGTTGAGTGGCGAGTTTCGAA 158  
QY 145 TCTGCCAGACCCACCAATTTGCTGGGCGCATAGCTCAGCTGGGAGAGCGCCCTGCTTGC 204  
|||||  
Db 159 TCTCCAGACCCACCAA--GAACGGGGCATAGCTCAGTTGGTAGAGCACCTGCTTGC 216  
QY 205 AGCAGAGGTGAGGTTGATCCGCTGGCTCCACACCCCGCTTGCAGTTTGTCA 264  
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Db 217 AAGCAGGGGTGATCGATCCGCTTGGCTCCACCAAACTTTACAAATGAAAGCA 276  
QY 265 AAGCTTAGAAATGAATATTCGCGTGAATATTGATTTCGAACTTTATCAGATCGTTCT 324  
Db 277 AGTTTCTGTTTACGAGCTTATTTGATTTCGAGTAGAATAGCAGCATCATCT 336  
QY 325 TTAATAATTTGGTATGATAGAAAGATAGACTGGACAGCACTTTCACTGGTGTGT 383  
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Db 337 TTAACAAATTTGAAAGCCGAAATCAACAAAGACAAATGAGTTGTTTGTATTTT 395

RESULT 14  
US-08-635-761-86

Sequence 86, Application US/08635761  
Patent No. 5945282  
GENERAL INFORMATION:  
APPLICANT: Rossau, Rudi  
TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
STREET: 3100 No. 5945282 West Center, 90 S. 7th Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: U.S.A.  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/635,761  
FILING DATE: 19-APR-1996  
CLASSIFICATION: 435

us-09-931-486-115.rni

Mon Feb 3 16:49:19 2003

FILING DATE: 19-APR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: 07/965,394  
FILING DATE: 17-DEC-1992  
APPLICATION NUMBER: 08/412,614  
FILING DATE: 29-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A  
REGISTRATION NUMBER: 31,838  
REFERENCES/DOCKET NUMBER: 8076.75USC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/332-5300  
TELEFAX: 612/332/9081

TELEX: 85:  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-09-312-520-85

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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,394  
FILING DATE: 17-DEC-1992  
APPLICATION NUMBER: 08/412,614  
FILING DATE: 29-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076.75USC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/332-5300  
TELEFAX: 612/332/9081  
TELEX:

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; INFORMATION FOR SEQ ID NO: 86:
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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 603 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-635-761-86

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RESULT 15
US-09-312-520-85
; Sequence 85, Application us/09312520
; Patent No. 6277577
; GENERAL INFORMATION:
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6277577west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312, 520

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Title: US-09-931-486-115

Perfect score: 468

Sequence: 1 ATCGACGACATCAGCTGTCT.....CAGATTGCTGGGTATAT 468

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
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11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
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14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	110.8	23.7	640681	10	US-09-790-988-1
2	109	23.3	603	10	US-09-863-086-85
3	109	23.3	603	10	US-09-863-086-86
4	100.8	21.5	549	10	US-09-863-086-92
5	99.4	21.2	498	10	US-09-863-086-90
6	93	19.9	243	10	US-09-815-242-1358
7	92.4	19.7	255	10	US-09-815-242-1377
8	92.4	19.7	255	10	US-09-815-242-1402
9	92.4	19.7	255	10	US-09-815-242-1415
10	92.4	19.7	255	10	US-09-815-242-1423
11	92.4	19.7	255	10	US-09-815-242-1431
12	92.4	19.7	255	10	US-09-815-242-1454
13	92.4	19.7	255	10	US-09-815-242-1473
14	92.4	19.7	255	10	US-09-815-242-1499
15	92.4	19.7	255	10	US-09-815-242-1544
16	92.4	19.7	255	10	US-09-815-242-1544
17	92.4	19.7	255	10	US-09-815-242-1638
18	89	19.0	582	10	US-09-863-086-87
19	89	19.0	590	10	US-09-863-086-88

20	87	18.6	654	10	US-09-863-086-89	Sequence 89, Appl
21	86.4	18.5	3309400	9	US-09-738-626-1	Sequence 1, Appl
c 22	82	17.5	9797	10	US-09-070-927A-550	Sequence 550, App
23	74	15.8	290	10	US-09-815-242-4692	Sequence 4692, Ap
c 24	74	15.8	495	10	US-09-815-242-2687	Sequence 2687, Ap
c 25	74	15.8	495	10	US-09-815-242-2691	Sequence 2691, Ap
26	72	15.4	2336	10	US-09-842-552-102	Sequence 102, App
27	71.8	15.3	246	10	US-09-863-086-95	Sequence 95, Appl
28	71.2	15.2	76	10	US-09-974-300-4361	Sequence 4361, Ap
29	71.2	15.2	76	10	US-09-974-300-4403	Sequence 4403, Ap
30	71.2	15.2	76	10	US-09-974-300-4409	Sequence 4409, Ap
31	71.2	15.2	76	10	US-09-974-300-4418	Sequence 4418, Ap
32	71.2	15.2	76	10	US-09-974-300-8396	Sequence 8396, Ap
33	71.2	15.2	76	10	US-09-974-300-8438	Sequence 8438, Ap
34	71.2	15.2	76	10	US-09-974-300-8444	Sequence 8444, Ap
35	71.2	15.2	76	10	US-09-974-300-8453	Sequence 8453, Ap
36	70.2	15.0	279	10	US-09-863-086-96	Sequence 96, Appl
37	69.2	14.8	74	10	US-09-974-300-4363	Sequence 4363, Ap
38	68.2	14.8	76	10	US-09-974-300-8398	Sequence 8398, Ap
c 39	68.2	14.6	1069	10	US-09-070-927A-869	Sequence 869, App
40	65.8	14.1	836	9	US-09-894-467-5	Sequence 5, Appl
41	64.4	13.8	108	12	US-10-046-722-9	Sequence 9, Appl
c 42	62	13.2	213	10	US-09-815-242-1374	Sequence 1374, Ap
c 43	62	13.2	213	10	US-09-815-242-1375	Sequence 1375, Ap
c 44	62	13.2	213	10	US-09-815-242-1376	Sequence 1376, Ap
c 45	62	13.2	213	10	US-09-815-242-1412	Sequence 1412, Ap

## ALIGNMENTS

### RESULT 1

US-09-790-988-1  
; Sequence 1, Application US/09790988  
; Patent No. US20020127687A1  
; GENERAL INFORMATION:  
; APPLICANT: SHIGENOBU, SHUJI  
; APPLICANT: WATANABE, HIDEKI  
; APPLICANT: HATTORI, MASAHIRO  
; APPLICANT: SAKAKI, YOSHIYUKI  
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
; FILE REFERENCE: 081356/0159  
; CURRENT APPLICATION NUMBER: US/09790,988  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: JP2000-107160  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 640681  
; TYPE: DNA  
; ORGANISM: Buchnera sp.  
US-09-790-988-1

Query Match	23.7%	Score 110.8;	DB 10;	Length 640681;
Best Local Similarity	79.0%;	Pred. No. 2.6e-24;		
Matches 147;	Conservative 0;	Mismatches 32;	Indels 7;	Gaps 1;
QY 63	ATTAGGTAGCAACCTTCGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATA 122			
Db 275618	ATTATCTAATAAAAAAATTAGAAAGGCTTGTAGCTCAGATGGTTAGAGCGCACCCCTGATA 275677			
QY 123	AGGTTAGGTCGGCAGTTCGAATCTGCCAGACCCACC-----AATTTGCTGGGGCCA 175			
Db 275678	AGGTTAGGTCGGTGGTTCAATTCACCTCAGGCCTTACCAATAAAAAATCATCTGGGGCTA 275737			
QY 176	TAGCTCAGTGGGAGAGCGCTTCCTTCGACGAGAGGTGAGCGGTTCGATCCGCGCTG 235			
Db 275738	TAGCTCAGTGGGAGAGCGCTTCCTTCGACGAGAGGTGAGCGGTTCGATCCGCGCTG 275797			
QY 236	GCTCCA 241			
Db 275798	GCTCCA 275803			

## RESULT 2

US-09-863-086-95  
; Sequence 85, Application US/09863086  
; Patent No. US20020048762A1  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
; REGION BETWEEN THE 16S A  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/863,086  
; FILING DATE: 22-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/312,520  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/412,614  
; FILING DATE: 29-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.75USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/332-5300  
; TELEFAX: 612/332-9081  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 85:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 603 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: <Unknown>  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 85:  
US-09-863-086-85

Query Match 23.3%; Score 109; DB 10; Length 603;  
Best Local Similarity 62.5%; Pred. No. 1.8e-25;  
Matches 187; Conservative 0; Mismatches 110; Indels 2; Gaps 1;

QY	85	GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGTTCGGCAGTTTCGAA	144
DB	99	GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGTTCGGCAGTTTCGAA	158
QY	145	TCCTCCAGAGAGTTCGATCCCGCTTGGTTCGATCCAGCCCGCTTCGCTTGC	204
DB	159	TCCTCCAGAGAGTTCGATCCCGCTTGGTTCGATCCAGCCCGCTTCGCTTGC	216
QY	205	ACGAGGAGTTCGATCCCGCTTGGTTCGATCCAGCCCGCTTCGCTTGC	264
DB	217	AAGCAGGAGTTCGATCCCGCTTGGTTCGATCCAGCCCGCTTCGCTTGC	276
QY	265	AAGCTTAGAATGAATATTCGCTCGAATATTTGATTTCTGAACCTTTATCAGATTCGTTCT	324
DB	277	AGTTTGTCTTTTAGCAGCTTATTTTGATTTTGGAGTAGAATACGACGATCGATCT	336

QY	325	TTAAATAATTTGGTGATGTGATAGAAAGATAGACTGCACAGCACTTTCACCTGGTGTGT	383
DB	337	TTAAACAATTTGGAAGCCGAATCAACAAACAAAGCAATGAGTTGTTGATTTTT	395

## RESULT 3

US-09-863-086-86  
; Sequence 86, Application US/09863086  
; Patent No. US20020048762A1  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER  
; REGION BETWEEN THE 16S A  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. US20020048762A1west Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/863,086  
; FILING DATE: 22-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/312,520  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/412,614  
; FILING DATE: 29-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.75USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/332-5300  
; TELEFAX: 612/332/9081  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 603 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: <Unknown>  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:  
US-09-863-086-86

Query Match 23.3%; Score 109; DB 10; Length 603;  
Best Local Similarity 62.5%; Pred. No. 1.8e-25;  
Matches 187; Conservative 0; Mismatches 110; Indels 2; Gaps 1;

QY	85	GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGTTCGGCAGTTTCGAA	144
DB	99	GGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAGAGGTGAGTTCGGCAGTTTCGAA	158
QY	145	TCCTCCAGAGAGTTCGATCCCGCTTGGTTCGATCCAGCCCGCTTCGCTTGC	204
DB	159	TCCTCCAGAGAGTTCGATCCCGCTTGGTTCGATCCAGCCCGCTTCGCTTGC	216
QY	205	ACGAGGAGTTCGATCCCGCTTGGTTCGATCCAGCCCGCTTCGCTTGC	264
DB	217	AAGCAGGAGTTCGATCCCGCTTGGTTCGATCCAGCCCGCTTCGCTTGC	276







; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1402  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1402

Query Match 19.7%; Score 92.4; DB 10; Length 255;  
Best Local Similarity 66.5%; Pred. No. 2.7e-20;  
Matches 153; Conservative 0; Mismatches 66; Indels 11; Gaps 1;  
QY 10 ATCAGCTGTCTCATAGCTCCACAGCAATTCCTTTCATTCATTGTAAGAGACGATTAGCT 69  
DB 230 AACATCTTCTTCAGAGATGCGGAATAACGTGACATATTGTTCAATTTGTAATGTTG 171  
QY 70 TAGCAACCTTCGATTGGTCTGTAGCTCAGTTCAGTTCATTCATTGTAAGAGACGATTAG 129  
DB 170 TTCAATTCAAATTAATGGGCTATAGCTCAGCTGGTTAGAGCGACGCTGATAAGCGTGA 111  
QY 130 GTCGCGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178  
DB 110 GTCGCGTGTTCGAGTCCACTTAGGCCACCAATTAATTAATACCTATTATTTGGGGCTTAG 51  
QY 179 CTCAGCTGGGAGAGCGCTTCCTTGCACGAGGAGTTCAGCGGTTTCGATC 228  
DB 50 CTCAGCTGGGAGAGCGCTTCCTTGCACGAGGAGTTCAGCGGTTTCGATC 1

RESULT 9  
US-09-815-242-1415/c  
; Sequence 1415, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1415  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1415

Query Match 19.7%; Score 92.4; DB 10; Length 255;  
Best Local Similarity 66.5%; Pred. No. 2.7e-20;  
Matches 153; Conservative 0; Mismatches 66; Indels 11; Gaps 1;  
QY 10 ATCAGCTGTCTCATAGCTCCACAGCAATTCCTTTCATTCATTGTAAGAGACGATTAGCT 69  
DB 230 AACATCTTCTTCAGAGATGCGGAATAACGTGACATATTGTTCAATTTGTAATGTTG 171  
QY 70 TAGCAACCTTCGATTGGTCTGTAGCTCAGTTCAGTTCATTCATTGTAAGAGACGATTAG 129  
DB 170 TTCAATTCAAATTAATGGGCTATAGCTCAGCTGGTTAGAGCGACGCTGATAAGCGTGA 111  
QY 130 GTCGCGAGTTCGAATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178  
DB 110 GTCGCGTGTTCGAGTCCACTTAGGCCACCAATTAATTAATACCTATTATTTGGGGCTTAG 51  
QY 179 CTCAGCTGGGAGAGCGCTTCCTTGCACGAGGAGTTCAGCGGTTTCGATC 228  
DB 50 CTCAGCTGGGAGAGCGCTTCCTTGCACGAGGAGTTCAGCGGTTTCGATC 1

RESULT 10  
US-09-815-242-1423/c  
; Sequence 1423, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1423  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-1423  
Query Match 19.7%; Score 92.4; DB 10; Length 255;  
Best Local Similarity 66.5%; Pred. No. 2.7e-20;



APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1459  
LENGTH: 255  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
US-09-815-242-1459

Query Match 19.7%; Score 92.4; DB 10; Length 255;  
Best Local Similarity 66.5%; Pred. No. 2.7e-20;  
Matches 153; Conservative 0; Mismatches 66; Indels 11; Gaps 1;

QY 10 ATCAGCTGCTCATAGTCCACAGCAATTCCTGATTCATTTGAAGACGATAGGT 69  
DB 230 AACATCTTCTCAGAGATGCGGAATACGTGACATATTTGATTCAGTTTGAATGTTG 171  
QY 70 TAGCAACCTTCGATGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGA 129  
DB 170 TTCATTCAAAATTAATGGGCTATAGCTCAGCTGGTTAGAGCGCACCCCTGATAAGGGTGA 111  
QY 130 GGTGGGAGTTCGATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178  
DB 110 GGTGGGAGTTCGATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 51  
QY 179 CTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTTCAGCGGTTTCGATC 228  
DB 50 CTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTTCAGCGGTTTCGATC 1

RESULT 14  
US-09-815-242-1473/c  
Sequence 1473, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
CURRENT APPLICATION NUMBER: US/09/815,242

APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1473  
LENGTH: 255  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
US-09-815-242-1473

Query Match 19.7%; Score 92.4; DB 10; Length 255;  
Best Local Similarity 66.5%; Pred. No. 2.7e-20;  
Matches 153; Conservative 0; Mismatches 66; Indels 11; Gaps 1;

QY 10 ATCAGCTGCTCATAGTCCACAGCAATTCCTGATTCATTTGAAGACGATAGGT 69  
DB 230 AACATCTTCTCAGAGATGCGGAATACGTGACATATTTGATTCAGTTTGAATGTTG 171  
QY 70 TAGCAACCTTCGATGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGA 129  
DB 170 TTCATTCAAAATTAATGGGCTATAGCTCAGCTGGTTAGAGCGCACCCCTGATAAGGGTGA 111  
QY 130 GGTGGGAGTTCGATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 178  
DB 110 GGTGGGAGTTCGATCTGCCAGACCCACCAAT-----TTGCTGGGGCCATAG 51  
QY 179 CTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTTCAGCGGTTTCGATC 228  
DB 50 CTCAGCTGGGAGAGCGCTGCTTGCACGAGGAGGTTCAGCGGTTTCGATC 1

RESULT 15  
US-09-815-242-1475/c  
Sequence 1475, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
CURRENT APPLICATION NUMBER: 60/257,931

Search completed: February 1, 2003, 07:10:52  
Job time : 238.042 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 01:09:56 ; Search time 873.271 Seconds  
(without alignments)  
8679.427 Million cell updates/sec

Title: US-09-931-486-115  
Perfect score: 468  
Sequence: 1 ATCGACGACATCAGCTGCT.....CAGATGCTTGGGTTATAT 468

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em_estin:*
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5: em_estov:*
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8: em_hic:*
9: gb_est1:*
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15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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c 2	187.6	40.1	629	17 BH201541	BH201541 Sml-57P13
c 3	165.2	35.3	639	17 AQ509640	AQ509640 nbxb0096P
4	117.2	25.0	319	10 BE092111	BE092111 IL2-BT073
5	80.4	17.2	497	13 BI544108	BI544108 S071 Grac
6	80.4	17.2	548	13 BI544155	BI544155 S129 Grac

7	78.8	16.8	539	13	BI544086
c 8	77.8	16.6	593	17	BH400944
c 9	77.8	16.6	760	17	BH393190
c 10	69.2	14.8	6499	17	BH771024
c 11	68.4	14.6	191	17	AZ578476
c 12	66.6	14.2	904	17	BH159957
c 13	65.8	14.1	577	17	BH819575
c 14	59.6	12.7	287	17	BH614410
c 15	59.6	12.7	754	17	BH405252
c 16	58.6	12.5	619	9	AA680996
c 17	57.6	12.3	3268	17	BH770998
c 18	55	11.8	615	17	CI16G5
c 19	55	11.8	690	17	CI19B2
c 20	54.4	11.6	608	17	BH375641
c 21	54.4	11.6	696	17	BH383241
c 22	54.2	11.6	617	9	AI526132
c 23	54	11.5	712	17	BH397037
c 24	53.6	11.5	2149	17	AQ012191
c 25	53.2	11.4	713	13	BJ096963
c 26	52.8	11.3	579	17	BH375975
c 27	52.6	11.2	541	17	BH387664
c 28	51.8	11.1	679	13	BI263958
c 29	51.6	11.0	774	12	BG354849
c 30	51.4	11.0	715	17	BH375497
c 31	50.6	10.8	902	17	CNS06M5P
c 32	50.2	10.7	551	10	BE092053
c 33	50	10.7	653	13	BJ318992
c 34	49	10.5	874	17	CNS06GSM
c 35	48.4	10.3	432	13	BI941477
c 36	48.4	10.3	1258	17	BH770957
c 37	48.2	10.3	501	13	BJ313245
c 38	48	10.3	330	14	BQ205940
c 39	47.8	10.2	907	17	CNS06M2C
c 40	47.4	10.1	1061	17	CNS06MOV
c 41	47	10.0	612	17	AQ989869
c 42	46.6	10.0	372	10	BE092243
c 43	44.6	9.5	337	10	AW238775
c 44	44.6	9.5	381	10	AW238039
c 45	44.6	9.5	411	10	AW238064

#### ALIGNMENTS

RESULT 1  
BH200120/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BH200120  
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BH200120  
BH200120.1 GI:16370164  
GSS:  
Schistosoma mansoni.  
Schistosoma mansoni.  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.  
1 (bases 1 to 507)  
Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed ,N.M.  
Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sml BAC library for gene discovery and map construction  
Unpublished (2001)  
Other\_GSSs: Sml-57J2.TF  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
Seq primer: M13 For  
Class: BAC ends.

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FEATURES
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        /organism="Schistosoma mansoni"
        /strain="Puerto Rico"
        /db_xref="taxon:6183"
        /clone="Sml-57J2"
        /clone_lib="Sml"
        /note="Vector: pBelobAC11; Site_1: Hin dIII; Constructed
in the laboratory of Dr. Denis Le Paslier at the Fondation
Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma
mansoni agarose embedded DNA was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBelobAC11 digested with Hin dIII. The average insert size
is 100 kb. Total clone coverage: approx. 7.95 x the
haploid genome. Further information can be found in Le
Paslier et al. (2000) Construction and characterization of
a Schistosoma mansoni bacterial artificial chromosome
library. Genomics 65: 129 c 117 g 125 t
      BASE COUNT      136 a 129 c 117 g 125 t
      ORIGIN
        Query Match      40.8%; Score 190.8; DB 17; Length 507;
        Best Local Similarity 72.5%; Pred. No. 1.4e-48;
        Matches 342; Conservative 0; Mismatches 97; Indels 33; Gaps 6;
      QY 1 ATCCAGCAGCATCAGCTGTCTCATAGCTCCACACAGAAATGCTTGATTCATGAAGAAGA 60
      Db 485 ATCAAGACCTCAGCTTCTCATAGTCCACACAGAAATGCTTGATTCATTCGGAAGA 426
      QY 61 CGATTAGGTTAGCAACCTT-----CGATTGGGTCTGTAGCTCAGTGGTTAGAGCGCA 113
      Db 425 CGGATTGGGTTGAGACCCGAGAGTGCAGATTGGGTCTGTAGCTCAGTGGTTAGAGCGCA 366
      QY 114 CCCCTGATAAGGGTTCAGTGGGAGAGTGCAGATCTGCCAGACCCACCAATTTGC----- 167
      Db 365 CCCCTGATAAGGGTTCAGTGGGAGAGTGCAGATCTGCCAGACCCACCAATTTGC----- 306
      QY 168 -----TGGGGCCATAGCTCAGTGGGAGAGCGCCTGCCCTTGCCACGAGAGGT 215
      Db 305 GCCAGTGTCAAAATGGGCGCATAGCTCAGTGGGAGAGCGCCTGCCCTTGCCACGAGAGGT 246
      QY 216 CAGCGGTTTCGATCCCGCTTGGCTCCACACCCCGCTTGCCTTGCCACGAGAGGT 332
      Db 245 CAGGAGTTCGATCCCTCTTGGCTCCACCA--TCAACTCAGATCGCTGGAAGCTCAGAAA 188
      QY 276 TGAATATTCG-CGTCGAATATTGATTTCTGAACTTT--ATCAGAAATCGTTCTTTAAAAAT 332
      Db 187 TGAACATTTGGTAGTCAATGTTGATTTCTGGTCTTTGCCAGAACTGTTCTTTAAAAAT 128
      QY 333 TTGGGTATGTATAGAAAGATAGACTGGACACACTTTTCCAGTGGTGTGTTTCAGAGCTAA 392
      Db 127 TTGGGTATGTATAGAAAGATAGACTGGACACACTTTTCCAGTGGTGTGTTTCAGAGCTAA 392
      QY 393 GGTAAATTTTGTAGTAATTAACAAGTTTTCGGCGGAATTTTCGGCGGAATGTCGCTTCAAGG 71
      Db 70 CAAAATTTGCGAGTTCAGCGCGGAATTTTCGGCGGAATGTCGCTTCAAGGTTA 19
      RESULT 2
      BH201541 629 bp DNA linear GSS 24-OCT-2001
      LOCUS Sml-57P13.TF Sml Schistosoma mansoni genomic clone Sml-57P13, DNA
      DEFINITION sequence.
      ACCESSION BH201541
      VERSION BH201541.1 GI:16373041
      KEYWORDS GSS.
      SOURCE Schistosoma mansoni.
      ORGANISM Schistosoma mansoni.
      Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
      Strigeiida; Schistosomatoidea; Schistosomatidae; Schistosoma.
      REFERENCE 1 (bases 1 to 629)
      AUTHORS Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed
      ,N.M.

```

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TITLE
  JOURNAL
  COMMENT
    Use of end sequences from Schistosoma mansoni (Puerto Rico strain)
    Sml BAC library for gene discovery and map construction
    Unpublished (2001)
    Other_GSSs: Sml-57P13.TF
    Contact: Najib M. El-Sayed
    Department of Eukaryotic Genomics
    The Institute for Genomic Research
    9712 Medical Center Dr., Rockville, MD 20850, USA
    Tel: 301 838 0200
    Fax: 301 838 0208
    Email: nelsayed@tigr.org
    lo.edu).
    Seq primer: M13 For
    Class: BAC ends.
  FEATURES
    source
      Location/Qualifiers
        1..629
          /organism="Schistosoma mansoni"
          /strain="Puerto Rico"
          /db_xref="taxon:6183"
          /clone="Sml-57P13"
          /clone_lib="Sml"
          /note="Vector: pBelobAC11; Site_1: Hin dIII; Constructed
in the laboratory of Dr. Denis Le Paslier at the Fondation
Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma
mansoni agarose embedded DNA was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBelobAC11 digested with Hin dIII. The average insert size
is 100 kb. Total clone coverage: approx. 7.95 x the
haploid genome. Further information can be found in Le
Paslier et al. (2000) Construction and characterization of
a Schistosoma mansoni bacterial artificial chromosome
library. Genomics 65: 87-94."
        BASE COUNT      157 a 172 c 146 g 154 t
        ORIGIN
          Query Match      40.1%; Score 187.6; DB 17; Length 629;
          Best Local Similarity 72.0%; Pred. No. 1.6e-47;
          Matches 340; Conservative 0; Mismatches 99; Indels 33; Gaps 6;
        QY 1 ATCCAGCAGCATCAGCTGTCTCATAGCTCCACACAGAAATGCTTGATTCATGAAGAAGA 60
        Db 485 ATCCAGACATTCAGCTTCTTCATAAGTTCCTCCACAGAAATGCTTGATTCATTCGGAAGA 426
        QY 61 CGATTAGGTTAGCAACCTT-----CGATTGGGTCTGTAGCTCAGTGGTTAGAGCGCA 113
        Db 425 CGGATTGGGTTGAGACCCGAGAGTGCAGATTGGGTCTGTAGCTCAGTGGTTAGAGCGCA 366
        QY 114 CCCCTGATAAGGGTTCAGTGGGAGAGTGCAGATCTGCCAGACCCACCAATTTGC----- 167
        Db 365 CCCCTGATAAGGGTTCAGTGGGAGAGTGCAGATCTGCCAGACCCACCAATTTGC----- 306
        QY 168 -----TGGGGCCATAGCTCAGTGGGAGAGCGCCTGCCCTTGCCACGAGAGGT 215
        Db 305 GCCAGTGTCAAAATGGGCGCATAGCTCAGTGGGAGAGCGCCTGCCCTTGCCACGAGAGGT 246
        QY 216 CAGCGGTTTCGATCCCGCTTGGCTCCACACCCCGCTTGCCTTGCCACGAGAGGT 332
        Db 245 CAGGAGTTCGATCCCTCTTGGCTCCACCA--TCAACTCAGATCGCTGGAAGCTCAGAAA 188
        QY 276 TGAATATTCG-CGTCGAATATTGATTTCTGAACTTT--ATCAGAAATCGTTCTTTAAAAAT 332
        Db 187 TGAACATTTGGTAGTCAATGTTGATTTCTGGTCTTTGCCAGAACTGTTCTTTAAAAAT 128
        QY 333 TTGGGTATGTATAGAAAGATAGACTGGACACACTTTTCCAGTGGTGTGTTTCAGAGCTAA 392
        Db 127 TTGGGTATGTATAGAAAGATAGACTGGACACACTTTTCCAGTGGTGTGTTTCAGAGCTAA 392
        QY 393 GGTAAATTTTGTAGTAATTAACAAGTTTTCGGCGGAATTTTCGGCGGAATGTCGCTTCAAGG 71
        Db 70 CAAAATTTGCGAGTTCAGCGCGGAATTTTCGGCGGAATGTCGCTTCAAGGTTA 19
      RESULT 3

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Matches 224; Conservative 0; Mismatches 38; Indels 54; Gaps 3;

QY 98 AGTTGTTAGAGCGACCCCTGATAAGGGTGGAGTGGCAGTTGGAATCTGCCAGACCC 157  
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 Db 1 AGTTGTTAGAGCGACCCCTGATAAGGGTGGAGTGGCAGTTGGAATCTGCCAGACCC 60  
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QY 158 ACCAATTTGCT-----GGGSCCATAGCTCAGCTGGGAGAGCG 194  
 |||||  
 Db 61 ACCAATTTGCTGGGGGAAAGCCCTGTAGAATACGGGGCCATAGCTCAGCTGGGAGAGCG 120  
 |||||

QY 195 CTGCGCTTGCAGCAGAGGTGACGGTTCGATCCCGCTTGGCTCCACCA-----244  
 |||||  
 Db 121 CCGCTTGCAGCAGAGGTGACGGTTCGATCCCGCTTGGCTCCACCAATTTAGCTGT 180  
 |||||

QY 245 -----CCCCGTTGCCAGTTTCAAGCTTAGAATCAATATTC-----284  
 |||||

Db 181 GATGGTTGTTGGCTGTAGTCTCTCGTTAGAGTTTGAAGATGAGCATTCATCATGCG 240  
 |||||

QY 285 -GCCTCGAATATTGATTTCTGAATCTATCAGAATCGTTCTTTAAAAATTTGGGTATGTG 343  
 |||||

Db 241 GATGGTGAATGTTGATTTCTAGTCTTTGATTAGATCGTTCTTTACAAATTTGGGTATGTG 300  
 |||||

QY 344 ATAGAAAGATAGACTG 359  
 |||||

Db 301 ATAGAAAGATAGACTG 316  
 |||||

RESULT 5  
 BI544108  
 LOCUS  
 DEFINITION S071 Gracilaria lemaneiformis gametophyte cDNA library Gracilaria lemaneiformis cDNA 5', mRNA sequence.

ACCESSION BI544108.1 GI:19033790  
 VERSION  
 EST.  
 KEYWORDS Gracilaria lemaneiformis.  
 SOURCE Gracilaria lemaneiformis.  
 ORGANISM Eukaryota; Rhodophyta; Florideophyceae; Gracilariiales; Gracilariaceae; Gracilaria.

REFERENCE 1 (bases 1 to 497)  
 Sun,X., Yang,G.P., Mao,Y.X. and Zhang,X.C.  
 Analysis of expressed sequence tags of a marine red alga, Gracilaria lemaneiformis  
 Unpublished (2001)  
 CONTACT: Sun, X.; Zhang, X. C.  
 College of Marine Life Sciences  
 Ocean University of Qingdao  
 Yushan Road 5, Qingdao, 266003, Shandong, China  
 Tel: +86-0532-2032789  
 Fax: +86-0532-2032276  
 Email: xc Zhang@ouqd.edu.cn

PCR PRIMERS  
 FORWARD: 5' -CGTGGTACCATGGTCTAGAGT-3'  
 BACKWARD: 5' -CTGATCTAGACCTGCAGGCTC-3'  
 Seq primer: 5' -CGTGGTACCATGGTCTAGAGT-3'  
 POLYA=No.

FEATURES  
 source  
 1..497  
 /organism="Gracilaria lemaneiformis"  
 /db\_xref="taxon:2778"  
 /clone\_lib="Gracilaria lemaneiformis gametophyte cDNA library"  
 /tissue\_type="gametophyte thalli"  
 /note="Vector: pMD 18-T; Site\_1: EcoR V with a T hang; Wild type Gracilaria lemaneiformis were harvested from Zhanshan Bay, Qingdao (China). After rinsed with boiled seawater, younger thalli was cut and washed every 3-4 days until 1 month. Then thalli was cultivated in Provasoli medium. Total RNA was isolated from thalli of gametophyte algae, using UNIQ-10 Trizol Total RNA Preparation Kit(Sangon Inc., Shanghai, China). The cDNA was synthesized, amplified and cloned using cDNA Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector

(Takara Biotechnology Co., Ltd., Dalian, China), respectively."

BASE COUNT 151 a 77 c 103 g 166 t

ORIGIN  
 Query Match 17.2%; Score 80.4; DB 13; Length 497;  
 Best Local Similarity 73.4%; Pred. No. 6.3e-14;  
 Matches 116; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

QY 85 GGGTCTGTAGCTCAGTTGGTTAGAGCGACCCCTGATAAGGGTGGAGTGGCAGTTGCGA 144  
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 Db 225 GGGCTATTAGCTCAGTTGGTTAGAGCGACCCCTGATAAGGGTGGAGTGGCTGTTCAA 284  
 |||||

QY 145 TCTGCCAGACCCACCA-ATTGCTGGGGCCATAGCTCAGCTGGGAGAGCCCTGCCTTG 203  
 |||||  
 Db 285 TCCAGGATAGCCACCACCATGAATAAGGGGTATAGCTCAGCTGGTAGAGCGCTGCTTTTG 344  
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QY 204 CAGCAGGAGGTGAGCGGTTGATCCCGCTTGGCTCCA 241  
 |||||

Db 345 CAAGGCAGATGTGAGCGGTTCAAAATCCGCTTATCTCCA 382  
 |||||

RESULT 6  
 BI544155  
 LOCUS  
 DEFINITION S129 Gracilaria lemaneiformis gametophyte cDNA library Gracilaria lemaneiformis cDNA 5', mRNA sequence.

ACCESSION BI544155.1 GI:19033837  
 VERSION  
 EST.  
 KEYWORDS Gracilaria lemaneiformis.  
 SOURCE Gracilaria lemaneiformis.  
 ORGANISM Eukaryota; Rhodophyta; Florideophyceae; Gracilariiales; Gracilariaceae; Gracilaria.

REFERENCE 1 (bases 1 to 548)  
 Sun,X., Yang,G.P., Mao,Y.X. and Zhang,X.C.  
 Analysis of expressed sequence tags of a marine red alga, Gracilaria lemaneiformis  
 Unpublished (2001)  
 CONTACT: Sun, X.; Zhang, X. C.  
 College of Marine Life Sciences  
 Ocean University of Qingdao  
 Yushan Road 5, Qingdao, 266003, Shandong, China  
 Tel: +86-0532-2032789  
 Fax: +86-0532-2032276  
 Email: xc Zhang@ouqd.edu.cn

PCR PRIMERS  
 FORWARD: 5' -CGTGGTACCATGGTCTAGAGT-3'  
 BACKWARD: 5' -CTGATCTAGACCTGCAGGCTC-3'  
 Seq primer: 5' -CGTGGTACCATGGTCTAGAGT-3'  
 POLYA=Yes.

FEATURES  
 source  
 1..548  
 /organism="Gracilaria lemaneiformis"  
 /db\_xref="taxon:2778"  
 /clone\_lib="Gracilaria lemaneiformis gametophyte cDNA library"  
 /tissue\_type="gametophyte thalli"  
 /note="Vector: pMD 18-T; Site\_1: EcoR V with a T hang; Wild type Gracilaria lemaneiformis were harvested from Zhanshan Bay, Qingdao (China). After rinsed with boiled seawater, younger thalli was cut and washed every 3-4 days until 1 month. Then thalli was cultivated in Provasoli medium. Total RNA was isolated from thalli of gametophyte algae, using UNIQ-10 Trizol Total RNA Preparation Kit(Sangon Inc., Shanghai, China). The cDNA was synthesized, amplified and cloned using cDNA Synthesis Kit, cDNA PCR Library Kit and pMD 18-T vector (Takara Biotechnology Co., Ltd., Dalian, China), respectively."

BASE COUNT 183 a 92 c 107 g 166 t

ORIGIN

Db	111 GGGCTATTAGCTCAGTTGGTTAGACGCACCCCTGATAAGGTTAGGTCCTGGTTCAAA	125
Qy	145 TCTGCCAGACCCACCA-ATTGTCTGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCGCTTG	203
Db	126 TCCAGGATAGCCACCATGAATAAAGGGGTATAGCTCAGCTGGTAGAGTGCTGCTTTG	185
Qy	204 CACGACGAGGTACGCGTTCGATCCGCTTGGCTCCA	241
Db	186 CAGGCAGATGTCAGCGGTTCAAATCCGCTTATCTCCA	223
RESULT 8		
LOCUS	BH400944/c	
DEFINITION	AG-ND-158022.TF ND-TAM Anopheles gambiae genomic clone AG-ND-158022	
ACCESSION	BH400944	
VERSION	BH400944.1	
KEYWORDS	GSS.	
SOURCE	African malaria mosquito.	
ORGANISM	Anopheles gambiae	
REFERENCE	1 (bases 1 to 593)	
AUTHORS	Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.	
TITLE	Direct Submission of BAC-end sequences from Anopheles gambiae	
JOURNAL	Unpublished (2001)	
COMMENT	Other_GSSs: AG-ND-158022.TR Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 3543 Email: bjloftus@tigr.org This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest. Seq primer: M13 For Class: BAC ends.	
FEATURES	Location/Qualifiers	
source	1..593 /organism="Anopheles gambiae" /strain="PEST" /db_xref="taxon:7165" /clone="AG-ND-158022" /clone_lib="ND-TAM" /note="Vector: pECBAC1; Site_1: HindIII"	
BASE COUNT	119 a 157 c 118 g 199 t	
ORIGIN		
Query Match	16.6%; Score 77.8; DB 17; Length 593;	
Best Local Similarity	77.4%; Pred. No. 4.7e-13;	
Matches 120;	Conservative 0; Mismatches 32; Indels 3; Gaps 2;	
QY	91 GTAGCTCAGTTGGTTAGACGCACCCCTGATAAGGTTAGGTCGAGTCGAATCGCC	150
Ddb	574 GTAGCTCAGCTGGTTAGACCGGTACACTGATATGTAGAGGTGGCAGTTGAGCGCTGCC	515
QY	151 CAGACCCCAAT--TGTGGGGCCATAGCTCAGCTGG-GAGAGCGCTGCTTGCACG	207
Ddb	514 CGAGACTACTAATTCAGAAAAGGGGAATAGCTCAGCTGGCTAGAGCGCTGCTTGCACG	455
QY	208 CAGGAGGTACGCGGTTCCATCCCGTTGGCTCCAC	242

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Db 454 CAGGAGTCAAGGTTGACTCCCTATTCTCCAC 420
RESULT 9
BH393190/c
LOCUS
DEFINITION AG-ND-168H12.TR ND-TAM Anopheles gambiae genomic clone AG-ND-168H12
, DNA sequence.
ACCESSION BH393190
VERSION BH393190.1 GI:17339331
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 760)
AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: AG-ND-168H12.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
(DNA). All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 Rev
Class: BAC ends.
FEATURES
source
location/Qualifiers
1..760
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone_lib="AG-ND-168H12"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
BASE COUNT 171 a 187 c 139 g 263 t
ORIGIN
Query Match 16.6%; Score 77.8; DB 17; Length 760;
Best Local Similarity 77.4%; Pred. No. 5.8e-13;
Matches 120; Conservative 0; Mismatches 32; Indels 3; Gaps 2;
QY 91 GTAGCTCAGTTGGTTAGAGCGCACCCCTGTGATAAGGTTGAGTTCGCGAGTTCGAATCTGCC 150
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 569 GTAGCTCAGCTGGTTAGAGCGCTACACTGATAATGTAGAGTTCGCGAGTTCGAGCTGCC 510
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 151 CAGACCCACCAATT--TGCTGGGCCATAGCTCAGCTGG-GAGAGCGCTCGCTTGCGAG 207
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 509 CGAGACTACTAATTGAAAAGGGGAATAGCTCAGCTGGTAGAGCGCTCGCTTGCGAG 450
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 208 CAGGAGGTCAGCGTTTCGATCCCGCTTGCTGCCAC 242
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 449 CAGGAGGTCAGGTTTCGACTCCCTTATTCCTCCAC 415
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
RESULT 10
BH771024
LOCUS
DEFINITION LLMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, DNA sequence.
ACCESSION BH771024

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BH771024.1 GI:20373981
GSS.
Lactococcus lactis subsp. cremoris.
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
REFERENCE 1 (bases 1 to 6499)
AUTHORS Bolotin,A., Ehrlich,S.D. and Sorokin,A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments, (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
Best homologue in strain ILL403 is ywgA (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.
FEATURES
source
location/Qualifiers
1..6499
/organism="Lactococcus lactis subsp. cremoris"
/strain="MG1363"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGMU2; Site_1: SmaI; Library of
chromosomal fragments of L.lactis strain MG1363 was
prepared by partial AluI digestion or by sonication."
BASE COUNT 1946 a 1228 c 1683 g 1642 t
ORIGIN
Query Match 14.8%; Score 69.2; DB 17; Length 6499;
Best Local Similarity 95.9%; Pred. No. 1.7e-09;
Matches 71; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 168 TGGGGCCATAGCTCAGCTGGGAGAGCGCCCTGCCTTCGACGAGGTCAGCGGTTCCAT 227
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 2164 TGGGGCCTTAGCTCAGCTGGGAGAGCGCCCTGCCTTCGACGAGGTCAGCGGTTCCAT 2223
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 228 CCGCTTGGCTCCA 241
||||| |||||||
Db 2224 CCGCTAGGCTCCA 2237
||||| |||||||
RESULT 11
AZ578476/c
LOCUS
DEFINITION AZ578476
191 bp DNA linear GSS 08-DEC-2000
sp. NGR234 genomic library of Rhizobium strain ANU265 Rhizobium
AZ578476
ACCESSION AZ578476
VERSION AZ578476.1 GI:11605796
KEYWORDS GSS.
SOURCE Rhizobium sp. NGR234.
ORGANISM Rhizobium sp. NGR234
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
REFERENCE 1 (bases 1 to 191)
AUTHORS Viprey,V., Rosenthal,A., Broughton,W.J. and Perret,X.
TITLE Genetic snapshots of the Rhizobium species NGR234 genome
JOURNAL Genome Biol. 1 (6), RESEARCH0014 (2000)
MEDLINE 2114532
COMMENT Contact: Virginie Viprey
Laboratoire de Biologie Molculaire des Plantes Supérieures
University of Geneva
1 Chemin de l'Imperatrice, Chambesy/Geneva 1292, Switzerland
Tel: +44(0)1603450000
Fax: +44(0)1603450045
Email: virginie.viprey@bbsrc.ac.uk
Class: shotgun.
FEATURES
source
location/Qualifiers
1..191

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/organism="Rhizobium sp. NGR234"
/strain="ANU265"
/db_xref="taxon:394"
/clone="23h03"
/clone_lib="Shot-gun genomic library of Rhizobium strain ANU265"
/notes="Vector: M13; derivative strain of NGR234 cured of PNGR234a"
BASE COUNT      47 a      62 c      44 g      37 t      1 others
ORIGIN
Query Match      14.6%; Score 68.4; DB 17; Length 191;
Best Local Similarity 78.6%; Pred. No. 1.7e-10;
Matches 81; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 151 CAGACCCACCAATTGCTGGGGCATAGCTCAGCTGGGAGAGCGCTGCCTTCACGCGAG 210
      |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 129 CAGATGATCGAAACGGTTGGGGCTGTAGCTCAGCTGGGAGAGACACNTGCTTTCAGACGAG 70
      |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 211 GAGGTCAGCGGTCGATCCCGCTTGCTGCCACCAACCCCGCTTG 253
      |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 69 GGGGTCAGCGGTCGATCCCGCTTCAGCTCCACCAATTCGATTG 27
      |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 12	BH159957	904 bp	DNA	linear	GSS 24-SEP-2001
LOCUS	BH159957/c				
DEFINITION	ENT513TF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.				
ACCESSION	BH159957				
VERSION	BH159957.1	GI:15733395			
KEYWORDS	GSS.				
SOURCE	Entamoeba histolytica.				
ORGANISM	Entamoeba histolytica.				
REFERENCE	Eukaryota; Entamoebidae; Entamoeba.				
AUTHORS	Loftus,B., Wang,Z., Van Aken,S. and Fraser,C.				
TITLE	Determination of clone end sequences from Entamoeba histolytica				
JOURNAL	HM1:IMSS sheared DNA library (2001)				
COMMENT	Unpublished (2001)				
	Contact: Brendan J Loftus				
	Department of Eukaryotic Genomics				
	The Institute for Genomic Research				
	9712 Medical Center Dr., Rockville, MD 20850, USA				
	Tel: 301 838 0208				
	Fax: 301 838 3543				
	Email: bjloftus@tigr.org				
	Clones are derived from the Entamoeba histolytica HM1:IMSS sheared				
	DNA library				
	Seq primer: M13-Forward				
	Class: shotgun				
	High quality sequence start: 34				
	High quality sequence stop: 576.				
	Location/Qualifiers				
	1..904				
	/organism="Entamoeba histolytica"				
	/strain="HM1:IMSS"				
	/db_xref="taxon:3759"				
	/clone_lib="Entamoeba histolytica Sheared DNA"				
	/note="Vector: pHOSt; Site_1: Bst I; Constructed at The				
	Institute for Genomic Research (TIGR), Rockville, MD.				
	Genomic DNA isolated from broth cultures of E. histolytica				
	using a method described by Clark and Diamond (Clark,				
	C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a				
	method for isolate identification. Exp. Parasitol.				
	77:450.). The DNA was mechanically sheared to give a				
	tight size distribution (~2 kb). The v + i method used for				
	the library construction is described in detail in Smith,				
	H.O. and Venter, J.C. (Making small insert libraries for				
	whole genome shotgun sequencing projects. In Genome				
	Sequencing: A Practical Approach, eds. M. Vaudin and B.				
	Barell, Oxford University Press, 1999)."				
FEATURES	304 a 166 c 96 q 338 t				
source					
BASE COUNT					

ORIGIN	Query Match	14.2%;	Score 66.6;	DB 17;	Length 904;
	Best Local Similarity	63.9%;	Pred. No. 2.2e-09;		
	Matches 117;	Conservative 0;	Mismatches 64;	Indels 2;	Gaps 1;
QY	62	GATTAGGTTAGCAACCTTCGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGAT	121		
Db	882	GATTAGGTGGTTCCCAAGTAAATAGGATTCTTAGCTAGTGGTGAGAGCACCGGGTTTCAT	823		
QY	122	AAGGGTGAAGTTCGGCATCTGCCAGACCCACCAATTGCTTGGGGCCATAGCTC	181		
Db	822	ACCGGGTAGTCCCGGGTTCGATTCCCTGAAGGTCCACATTTT--TGGGGGTATAGCTC	765		
QY	182	AGCTGGGAGAGCGCCCTGCCTTGACGACGAGGAGTTCAGCGTTCGATCCCGCTTGGCTCCA	241		
Db	764	AGTGGGAAGAGCATTGCGCTTGCAGCGAGGGGTCAGGAGTTTGATCTCCTTACTTCCA	705		
QY	242	CCA 244			
Db	704	CGA 702			
RESULT 13					
LOCUS	BH819575				
DEFINITION	BACPP13-E14.y Pristionchus pacificus BAC ends Pristionchus				
ACCESSION	BH819575				
VERSION	BH819575.1				
KEYWORDS	GSS.				
SOURCE	GSS.				
ORGANISM	Pristionchus pacificus.				
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;				
AUTHORS	Neodiplogasteridae; Pristionchus.				
	1 (bases 1 to 577)				
	Srinivasan,J., Sins,W., Lanz,C., Brand,A., Nandakumar,R., Raddatz				
	G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A., Jesse,T.,				
	Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.				
TITLE	A BAC-based genetic linkage map of the nematode Pristionchus				
JOURNAL	published (2002)				
COMMENT	Contact: Sommer RJ				
	Evolutionary Biology				
	Max-Planck-Institute for Developmental Biology				
	Spemannstr. 37-39, Tuebingen D-72076, Germany				
	Tel: 00497071601371				
	Fax: 00497071601498				
	Email: ralf.sommer@tuebingen.mpg.de				
	Class: BAC ends.				

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Class: BAC ends.
Location/Qualifiers
1..577
/organism="Pristionchus pacificus"
/strain="var. California"
/db_xref="taxon:54126"
/clone_lib="Pristionchus pacificus BAC ends"

BASE COUNT      129 a      142 c      139 g      167 t
ORIGIN

Query Match      14.1%; Score 65.8; DB 17; Length 577;
Best Local Similarity 78.2%; Pred. No. 2.7e-09;
Matches 79; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 168 TGGGCCATAGCTACGCTGGGAGAGCGGCTGCTTGCACGACGAGAGGTCAGCGGTTTCGAT 227
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Ddb 118 TGGGCTTAGCTACGCTGGGAGAGCGGCTGCATGCGCATGCAAGAGGTCAGCGGTTTCGAT 177
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 228 CCGCGTTGGCTCCACCACCCCGCTTGGCCAGTTTGTTCAAAGC 268
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Ddb 178 CCGCGTTAGCTCCACCAAAATTTCCAACCTCGCTGCAAGC 218
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14

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RESULT 14

BH614410  
LOCUS  
DEFINITION 1C22AG2 Subclones from overlapping BAC clones spanning the hrp cluster of Erwinia carotovora subsp. atroseptica Pectobacterium carotovorum subsp. atrosepticum genomic, DNA sequence.  
ACCESSION BH614410.1 GI:18078210  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Pectobacterium carotovorum subsp. atrosepticum.  
Pectobacterium carotovorum subsp. atrosepticum  
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Pectobacterium.

REFERENCE 1 (bases 1 to 287)  
AUTHORS Bell, K.S., Avrova, A.O., Hovleva, M.C., Cardle, L., Morris, W., De Jong, W., Toth, I.K., Waugh, R., Bryan, G.J. and Birch, P.R.J.  
TITLE Sample sequencing of a selected region of the genome of Erwinia carotovora subsp. atroseptica reveal candidate phytopathogenicity genes and allows comparison with Escherichia coli unpublished (2002)  
JOURNAL  
COMMENT Contact: Bell KS  
Scottish Crop Research Institute  
Invergowrie, Dundee, United Kingdom, DD2 5DA  
Email: kbells@scri.sari.ac.uk  
Class: BAC subclone.

FEATURES  
source Location/Qualifiers  
1..287  
/organism="Pectobacterium carotovorum subsp. atrosepticum"  
/strain="SCRI039"  
/db\_xref="taxon:29471"  
/clone\_lib="Subclones from overlapping BAC clones spanning the hrp cluster of Erwinia carotovora subsp. atroseptica"  
/note="Vector: pGEM 3zf; DNA from BAC clones Eca2B8 and Eca1C22 was nebulised and cloned into pGEM 3zf and sequenced with SP6 or T7 primers"

BASE COUNT 74 a 62 c 78 g 73 t  
ORIGIN  
Query Match 12.7%; Score 59.6; DB 17; Length 287;  
Best Local Similarity 78.9%; Pred. No. 1.4e-07;  
Matches 71; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 86 GGTCTGAGCTCAGTTGGTTAGAGCGCACCCCTGTAGAGGTGCGGAGTTCGAAT 145  
Db 174 GCTTTGAGCTCAGTTGGTTAGAGCGCACCCCTGTAGAGGTGCGGAGTTCGAAT 233  
Qy 146 CTGCCAGACCCACCAATTTGCTGGGGCA 175  
Db 234 CCACTCAGGCGCTACCAATTTGCACGGCAA 263

RESULT 15  
BH405252/C  
LOCUS  
DEFINITION AG-ND-127K13.TR ND-TAM Anopheles gambiae genomic clone AG-ND-127K13  
DNA linear GSS 11-DEC-2001  
DNA sequence.  
ACCESSION BH405252  
VERSION BH405252.1 GI:17351468  
KEYWORDS  
SOURCE  
ORGANISM African malaria mosquito.  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

REFERENCE 1 (bases 1 to 754)  
AUTHORS Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.  
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae  
JOURNAL  
COMMENT Unpublished (2001)  
Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543

Email: bjlouftus@tigr.org  
This clone is from an A. gambiae BAC library (ND-TAM) provided by F. H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.  
Seq primer: M13 Rev  
Class: BAC ends.

FEATURES  
source Location/Qualifiers  
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/organism="Anopheles gambiae"  
/strain="PEST"  
/db\_xref="taxon:7165"  
/clone\_lib="AG-ND-127K13"  
/clone\_lib="ND-TAM"  
/note="Vector: pECBAC1; Site\_1: HindIII"

BASE COUNT 180 a 199 c 167 g 208 t  
ORIGIN  
Query Match 12.7%; Score 59.6; DB 17; Length 754;  
Best Local Similarity 66.5%; Pred. No. 3e-07;  
Matches 129; Conservative 0; Mismatches 39; Indels 26; Gaps 2;  
Qy 77 CTTGATTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTAGAGGTGCGGTCGGC 136  
Db 645 CGTGGACTGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGTAGAGGTGCGGT 586  
Qy 137 AGTTCGAATCTGCCAGACCCACCAATTTGCT-----GGG 171  
Db 585 GGTTGAGGCCCACTAGACCCACCAAGATTCCAAATGTTGTTGTCGAGGATCCCCGGG 526  
Qy 172 GCCATAGCTCAGC-TGGGAGAGCGCTCGCTTGCACGAGGAGTCCAGGTTTCGATCCC 230  
Db 525 GGATTAGCTCAGCTTGGGAGAGCACCTGCTTTGCAAGCGGGGTCGTTTCGATCCC 466  
Qy 231 GCTTGGCTCCACCA 244  
Db 465 GTCATCCTCCACCA 452

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Job time : 878.271 secs